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Storkus et al.

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(54) **IMMUNOGENIC TUMOR ASSOCIATED STROMAL CELL ANTIGEN PEPTIDES AND METHODS OF THEIR USE**

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§ 371 (c)(1),

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PCT Pub. Date: **May 23, 2013**

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Related U.S. Application Data

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A61K 38/08 (2006.01)

A61K 38/17 (2006.01)

G01N 33/574 (2006.01)

A61K 39/00 (2006.01)

A61K 31/506 (2006.01)

(52) **U.S. Cl.**

CPC **A61K 45/06** (2013.01); **A61K 31/506** (2013.01); **A61K 38/08** (2013.01); **A61K 38/1709** (2013.01); **A61K 39/0011** (2013.01); **G01N 33/574** (2013.01); **G01N 33/5743**

(2013.01); **G01N 33/57438** (2013.01); **G01N 33/57446** (2013.01); **A61K 2039/5154** (2013.01); **A61K 2039/5158** (2013.01); **A61K 2039/5256** (2013.01); **A61K 2039/53** (2013.01); **A61K 2039/55538** (2013.01)

(58) **Field of Classification Search**

None

See application file for complete search history.

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(57) **ABSTRACT**

Immunogenic peptides from tumor associated stromal cell antigens, including combinations of such peptides, are disclosed herein. In some examples the peptides are useful for methods of eliciting an immune response. In additional examples the peptides are useful for methods of treating cancer. Methods for decreasing vascularization of a tumor using a Protein Delta Homolog 1 (DLK1) protein or a nucleic acid encoding the protein are also disclosed.

17 Claims, 27 Drawing Sheets

FIG. 1A

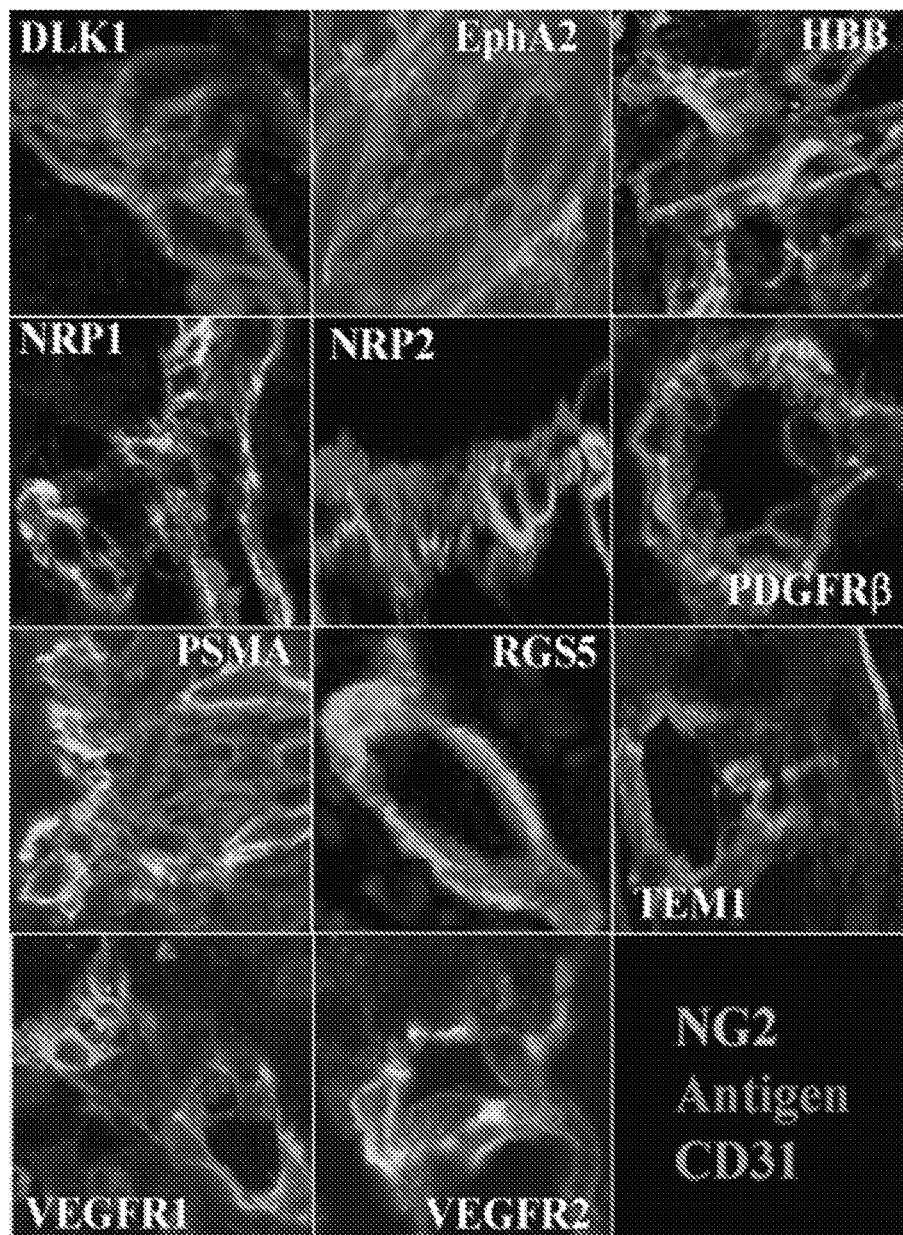


FIG. 1B

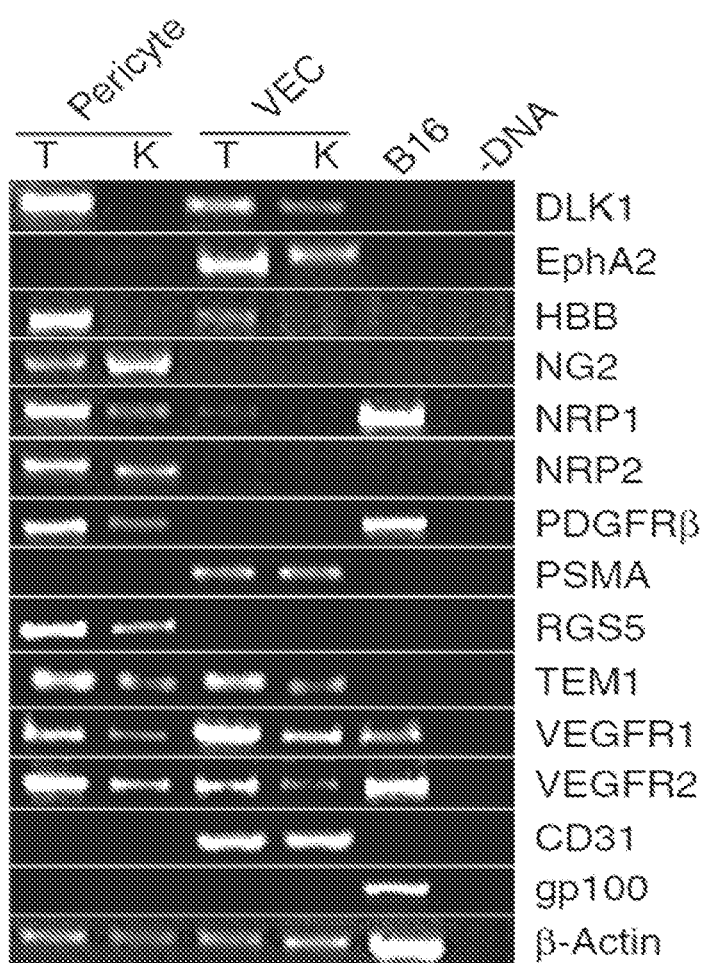


FIG. 2A

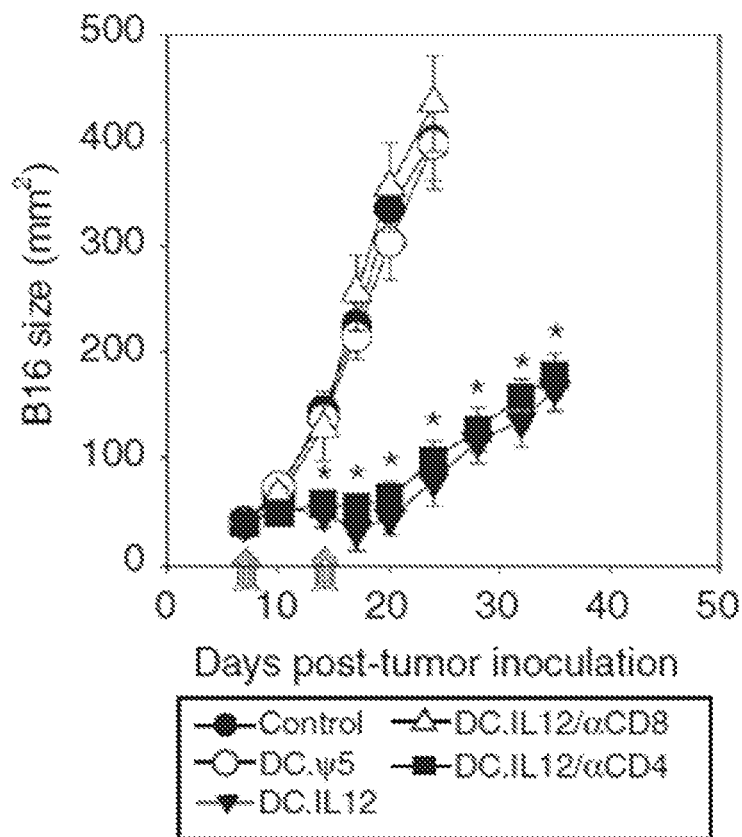


FIG. 2B

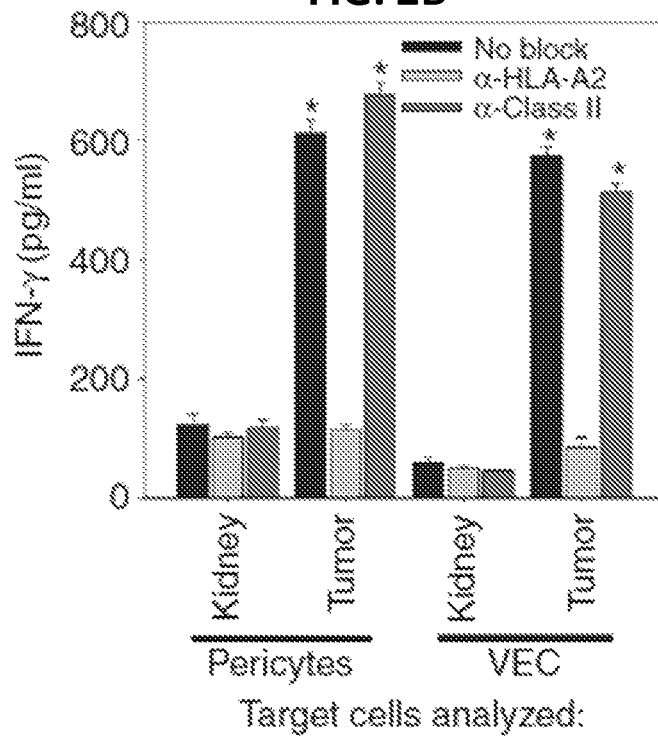


FIG. 2C

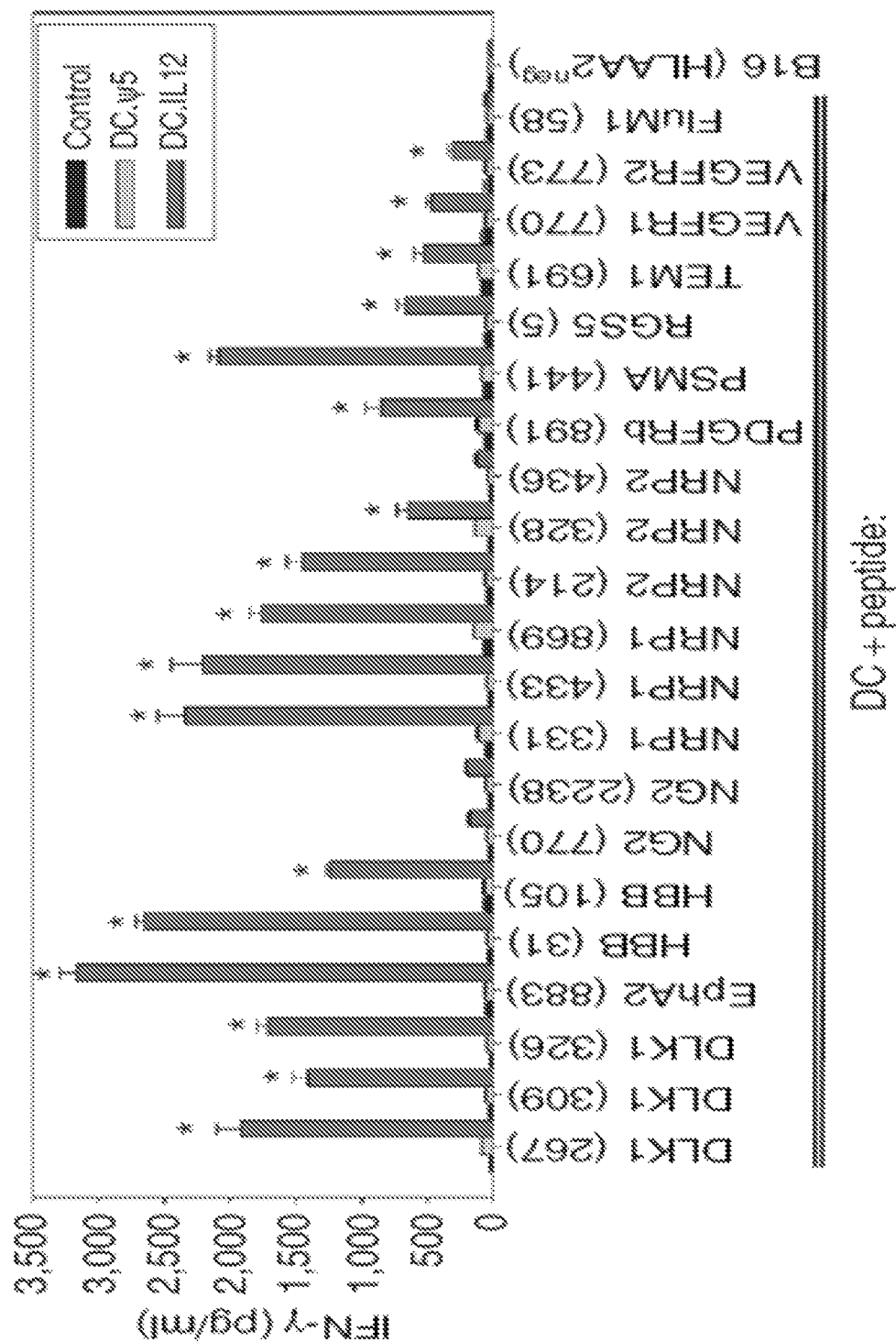


FIG. 3A

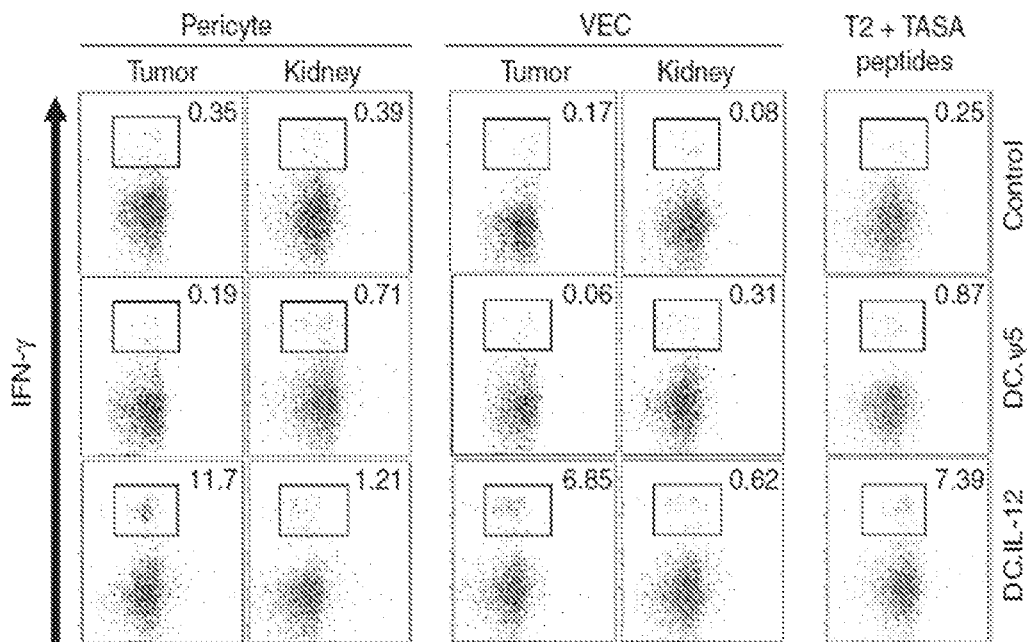


FIG. 3B

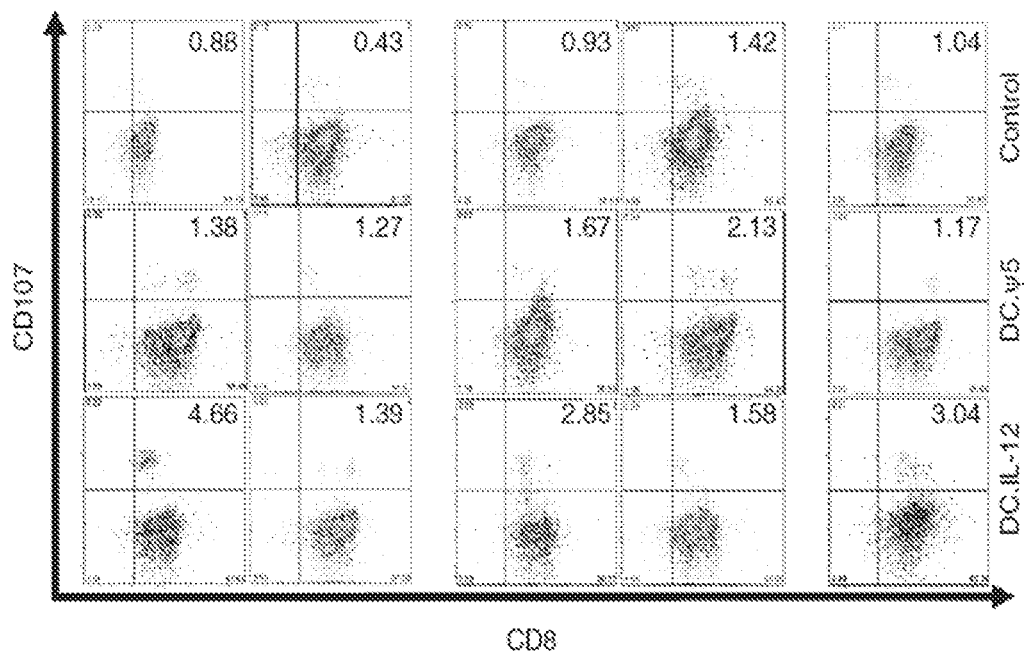


FIG. 4

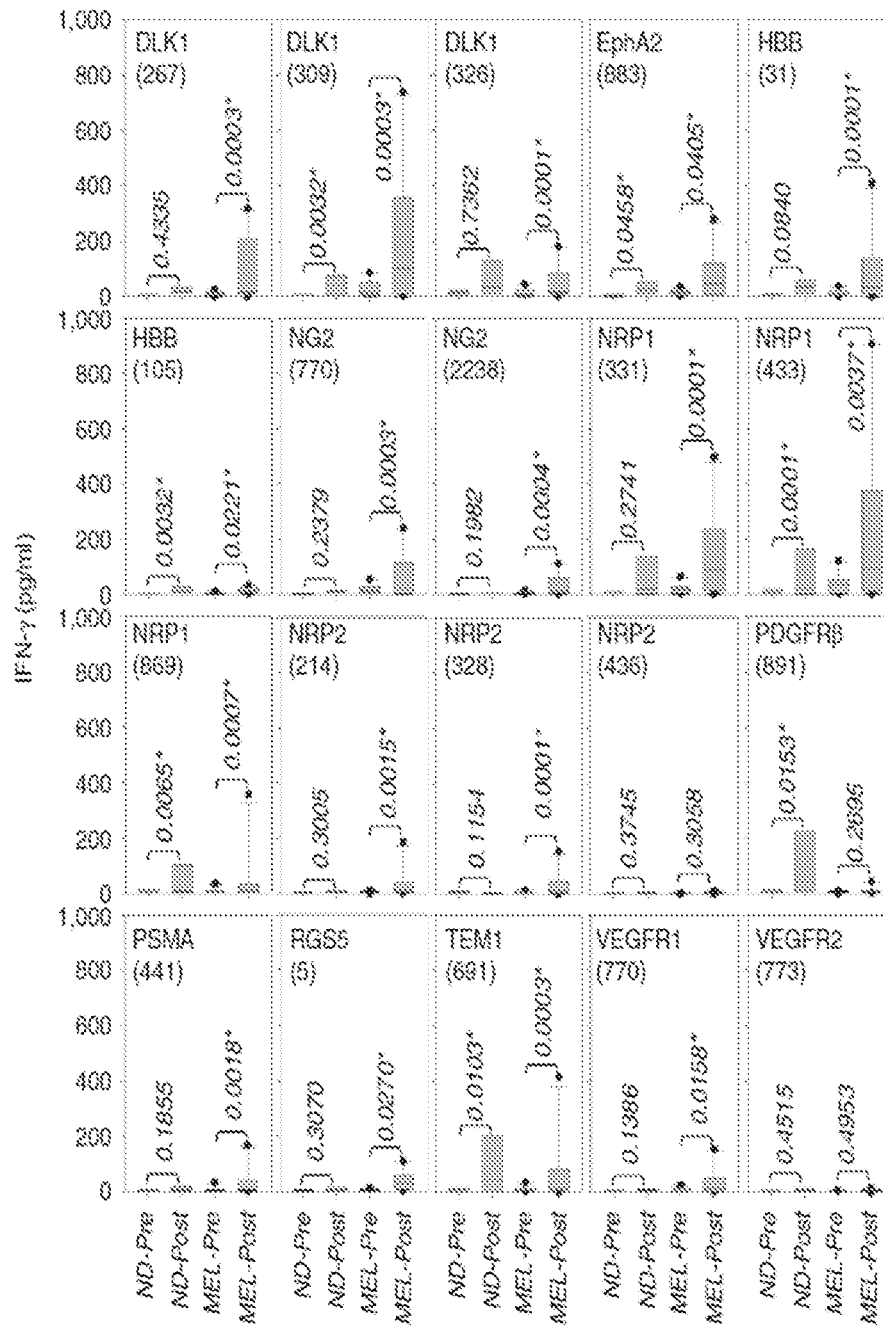


FIG. 5

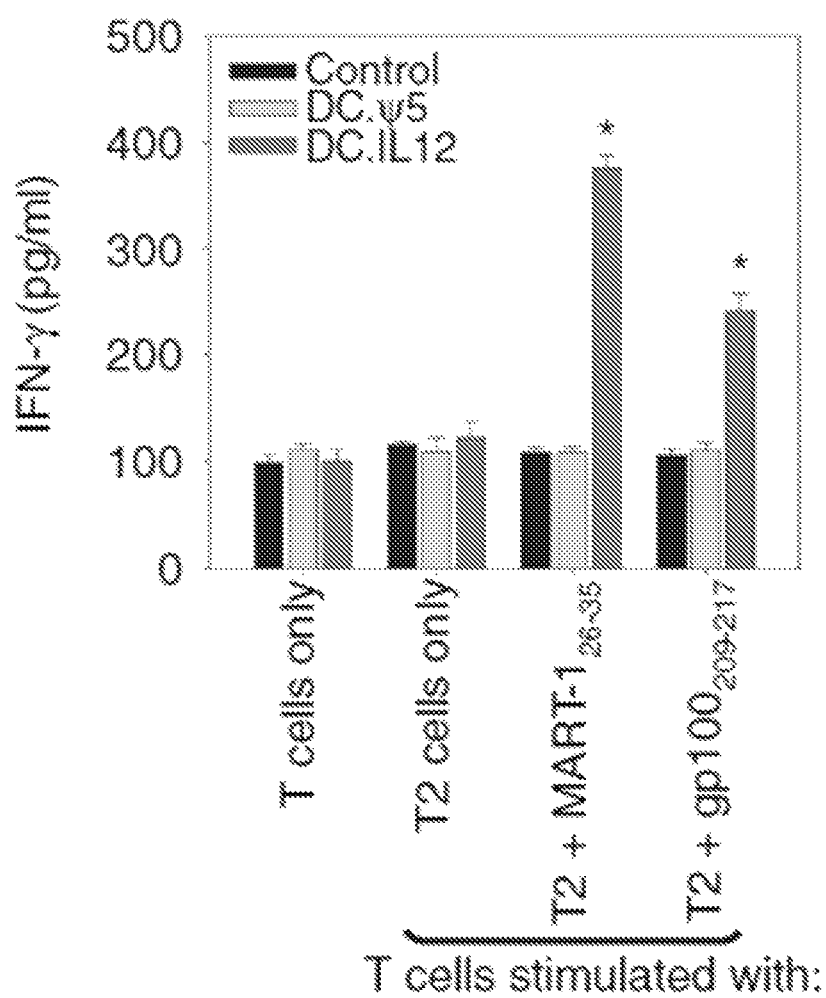


FIG. 6

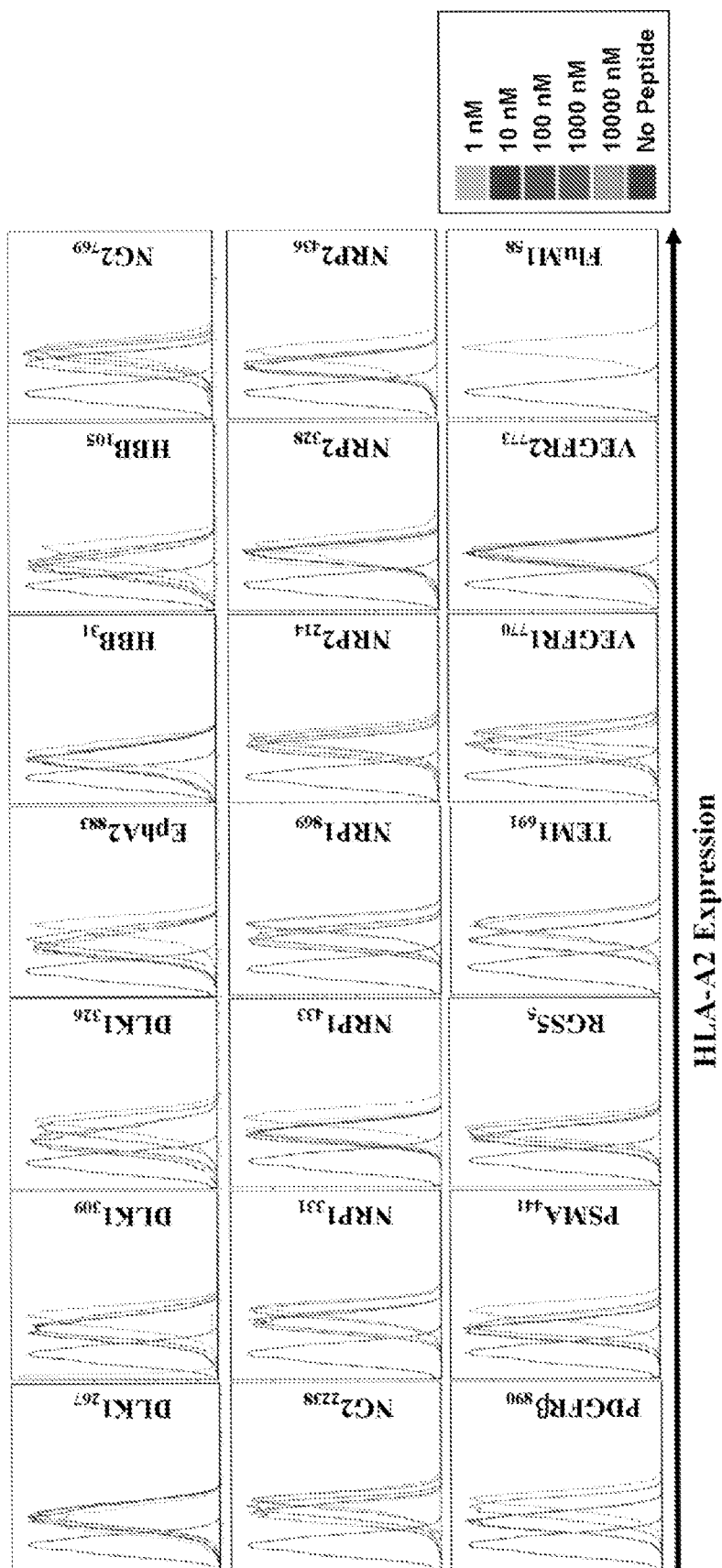


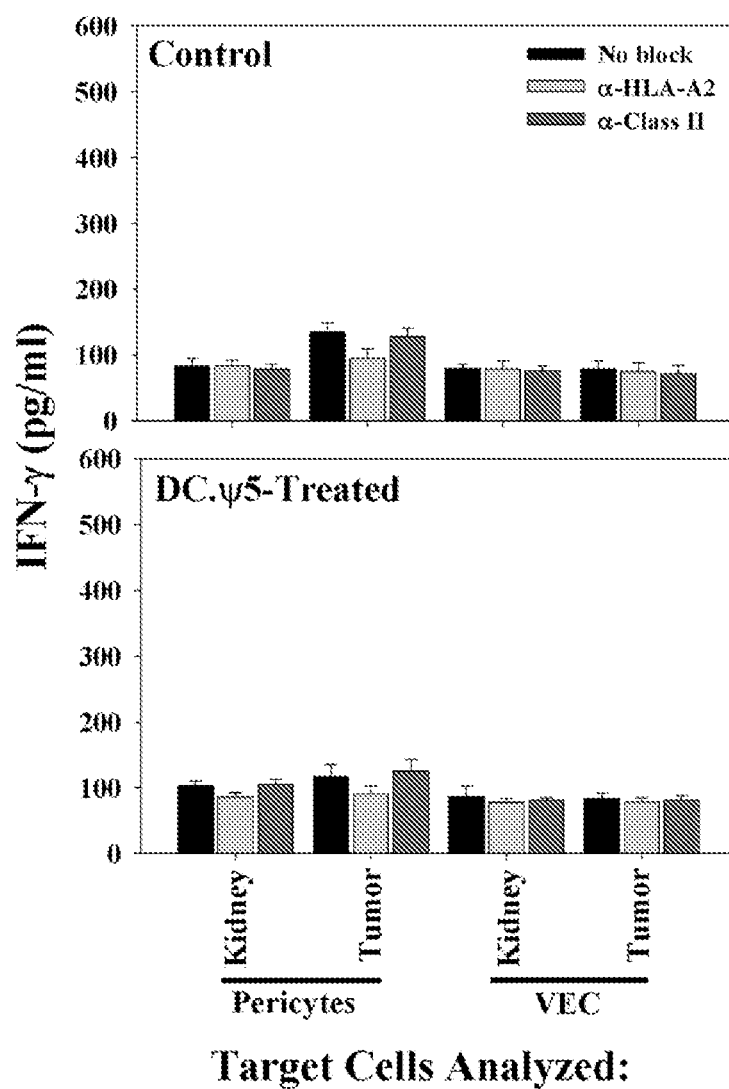
FIG. 7

FIG. 8A

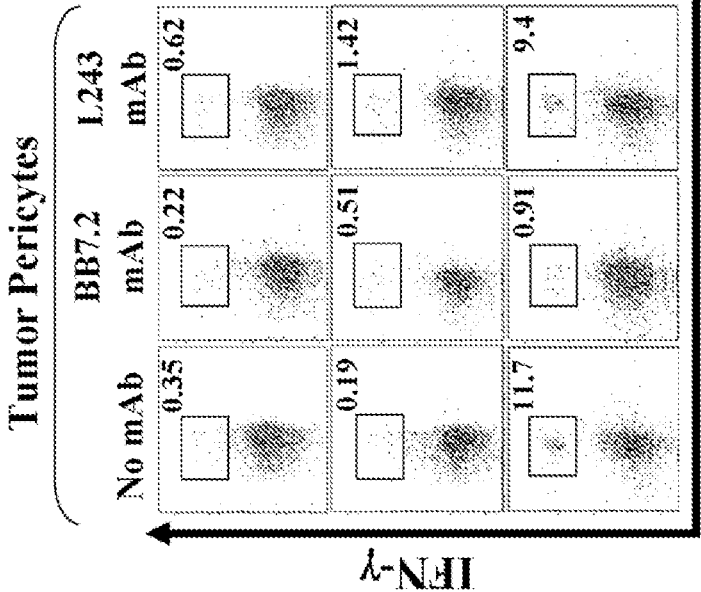


FIG. 8B

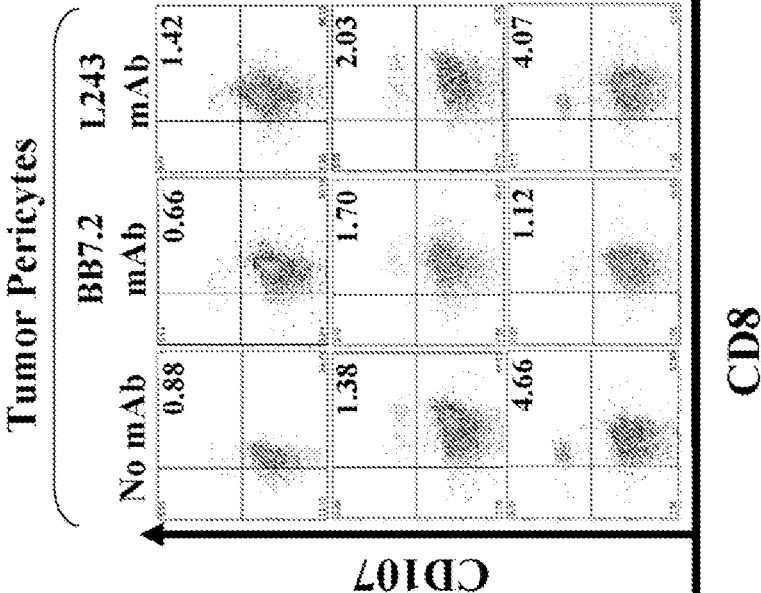


FIG. 8C

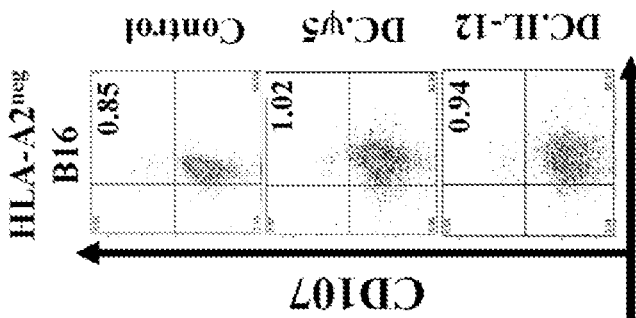


FIG. 9A

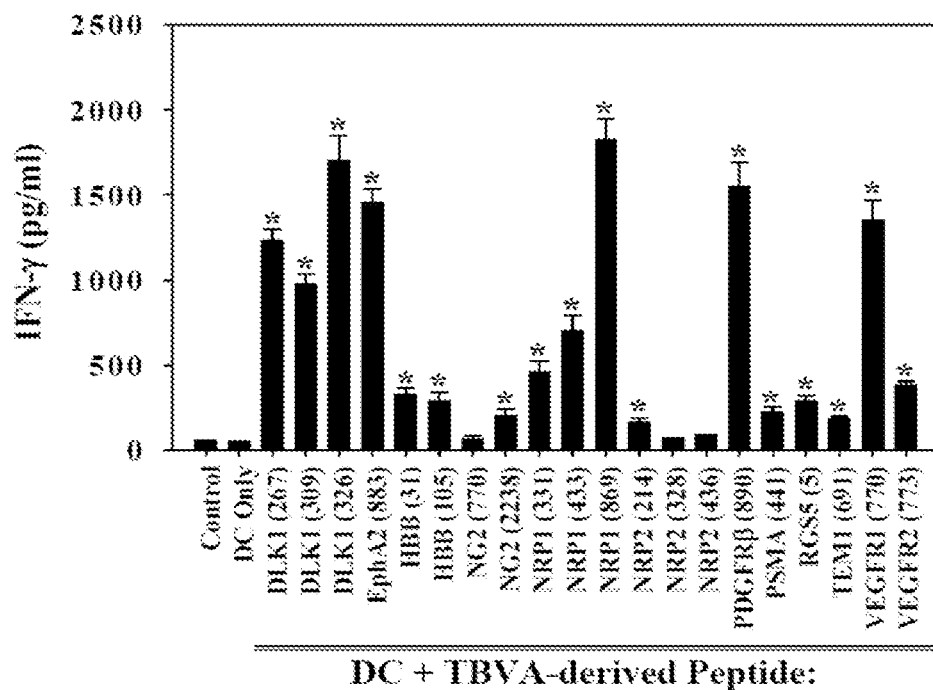


FIG. 9B

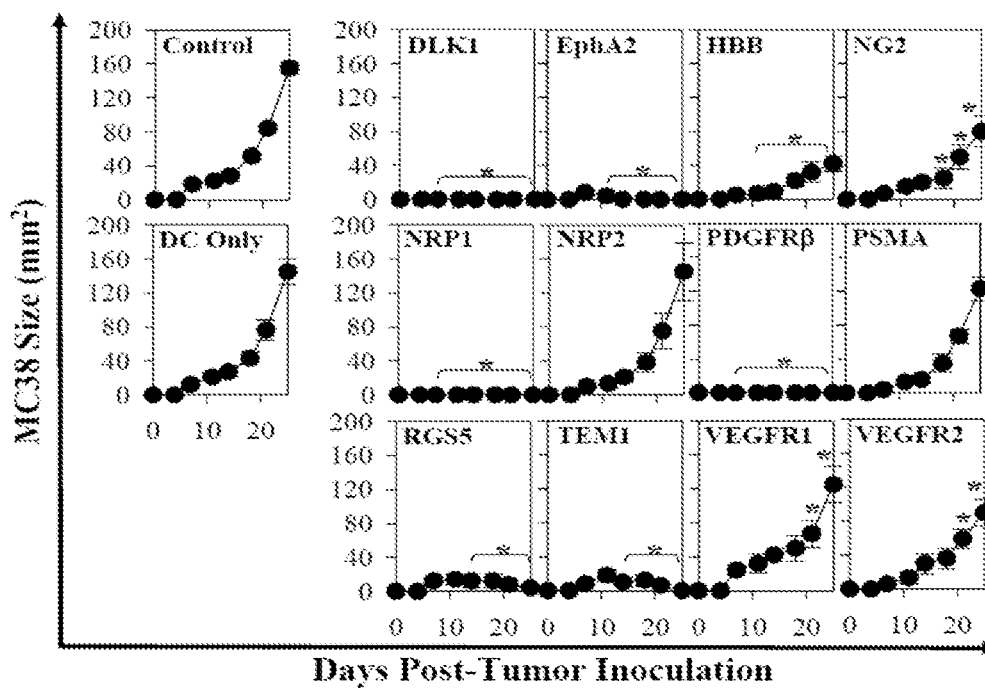


FIG. 10A

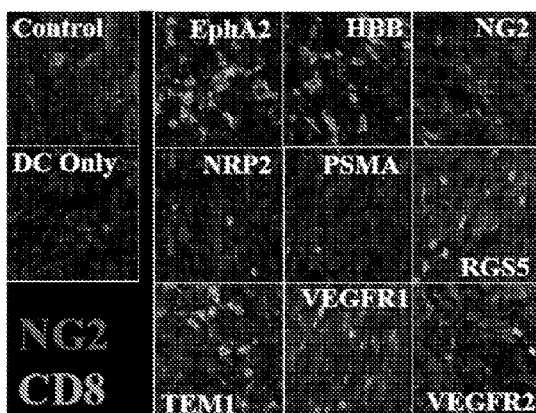


FIG. 10B

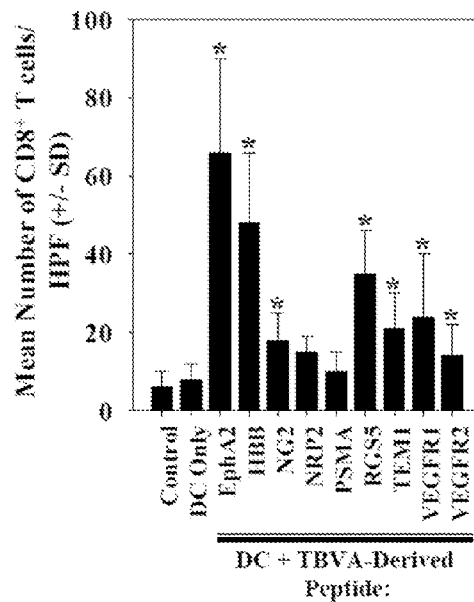


FIG. 10C

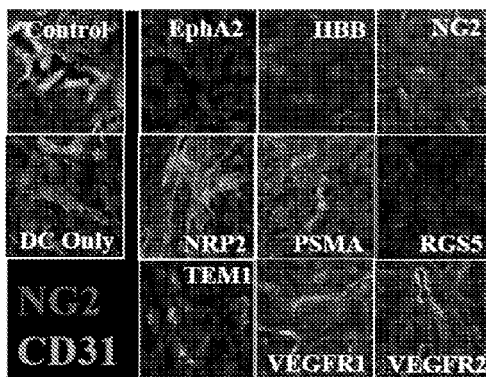


FIG. 10D

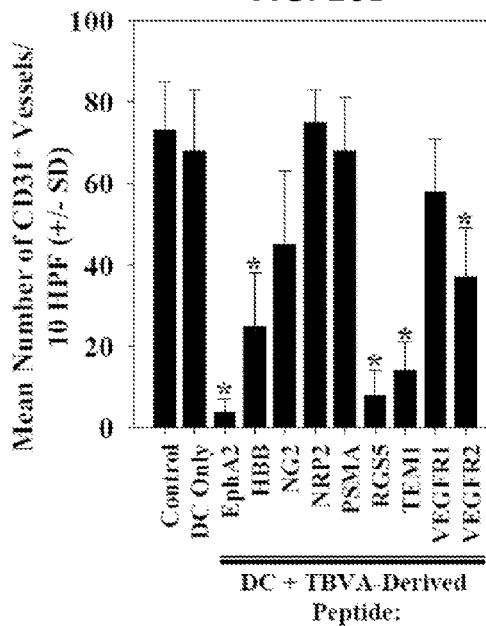


FIG. 11A

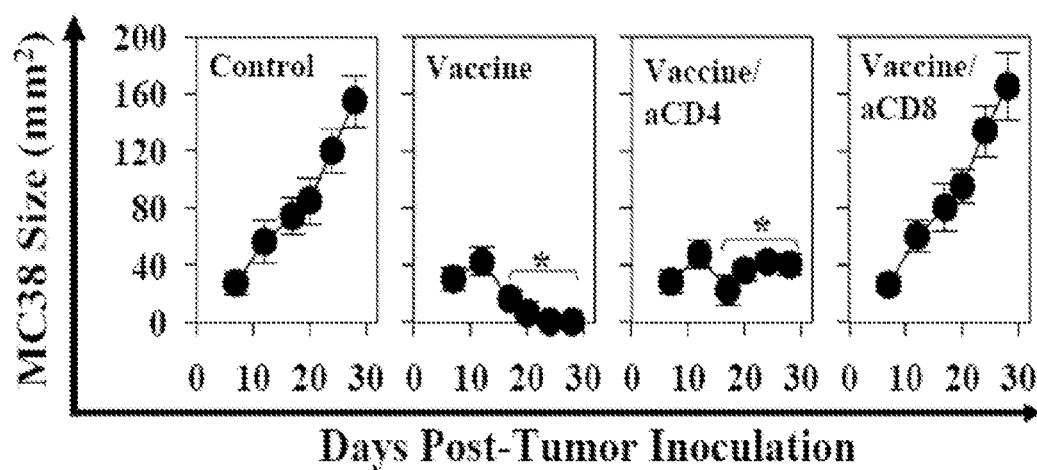


FIG. 11B

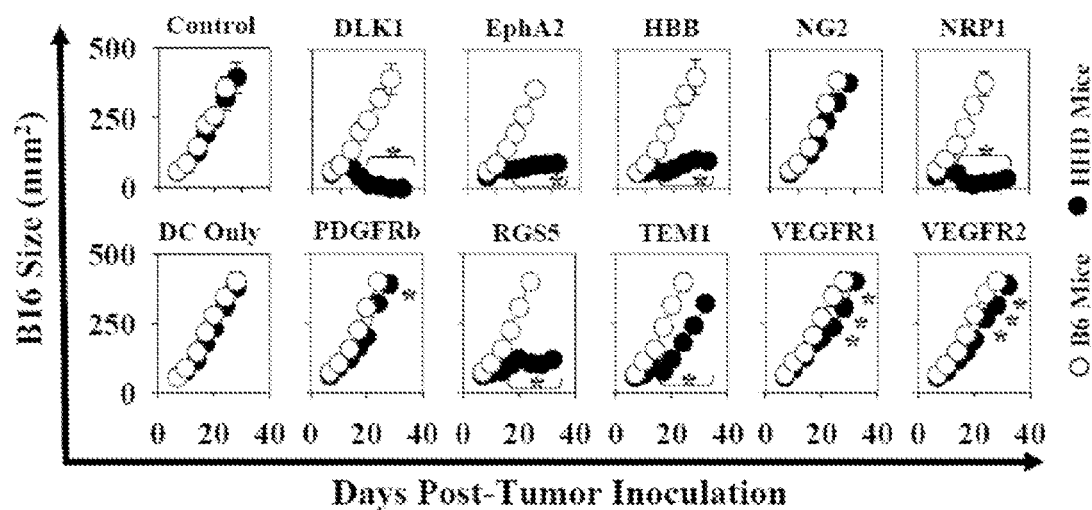


FIG. 11C

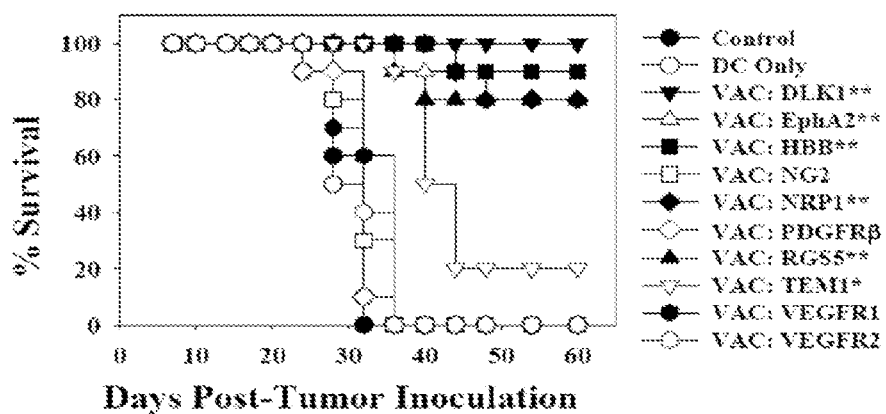


FIG. 12

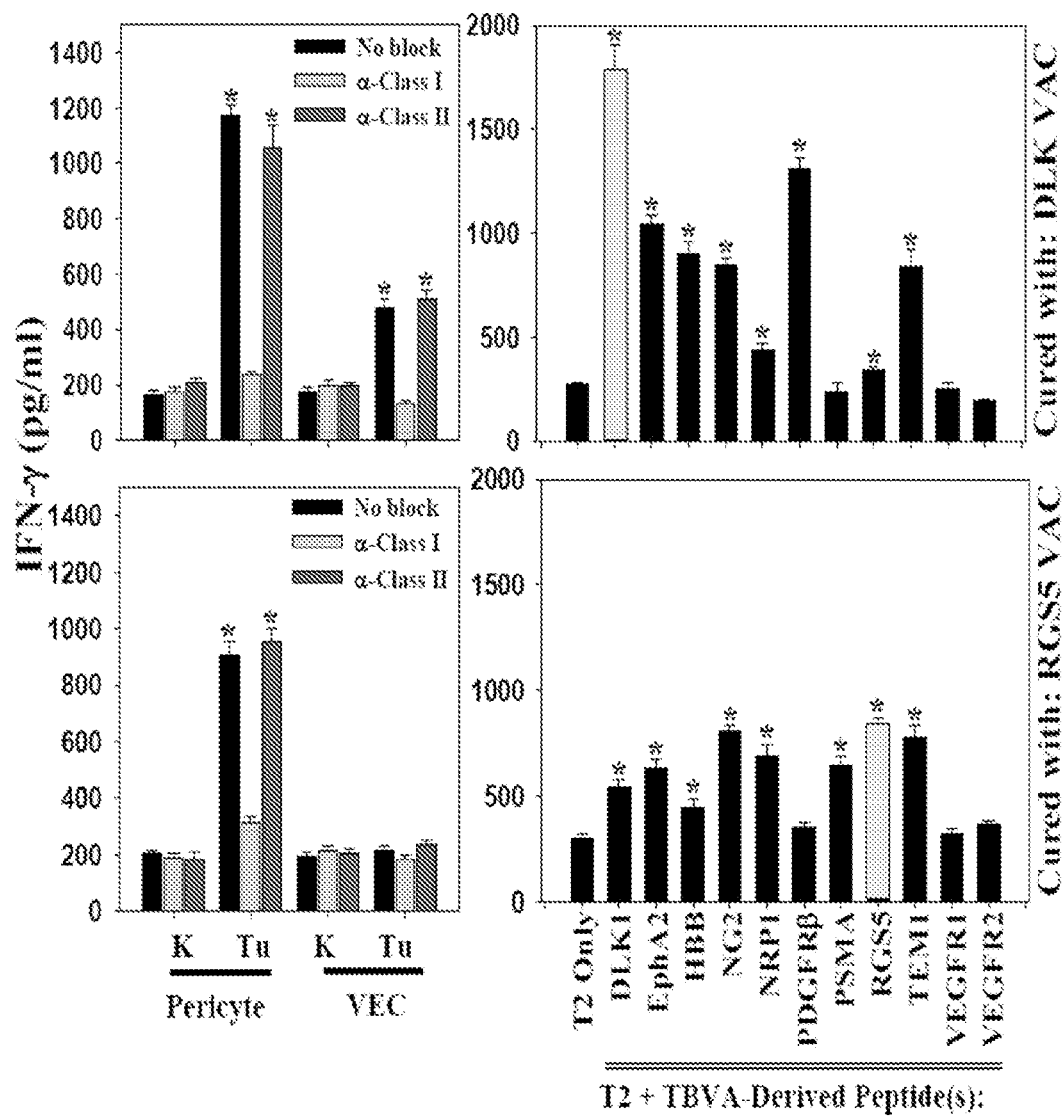


FIG. 13

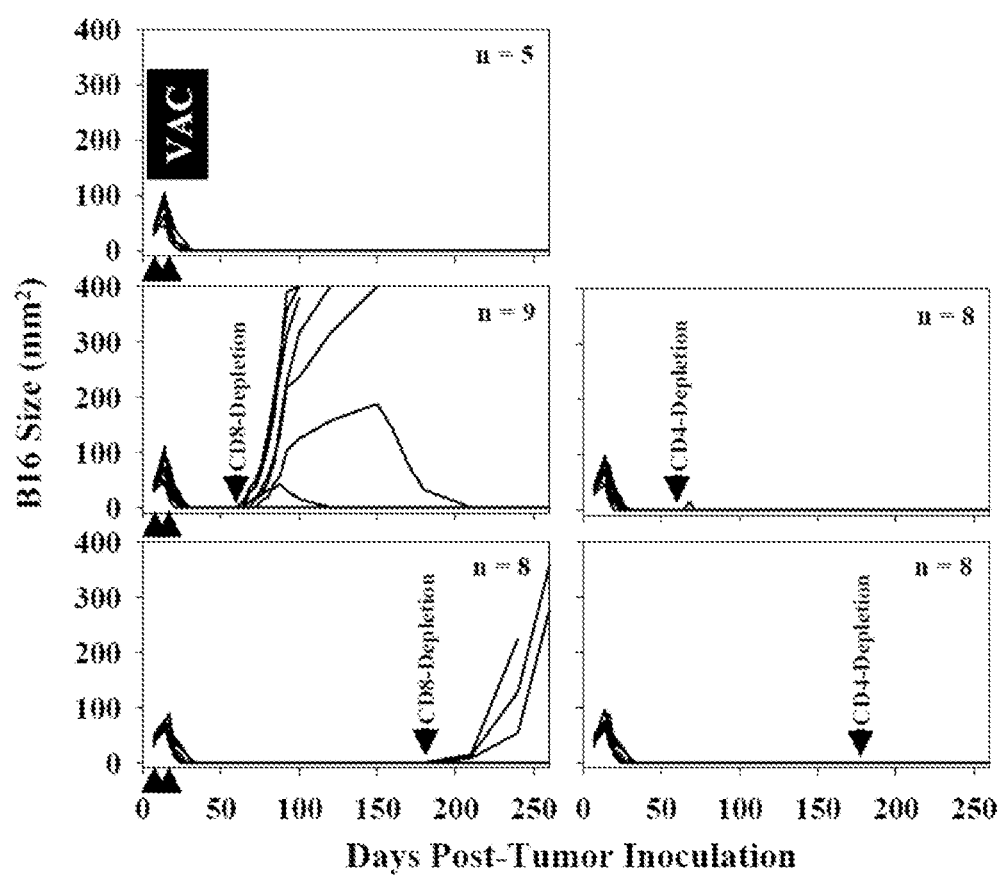


FIG. 14

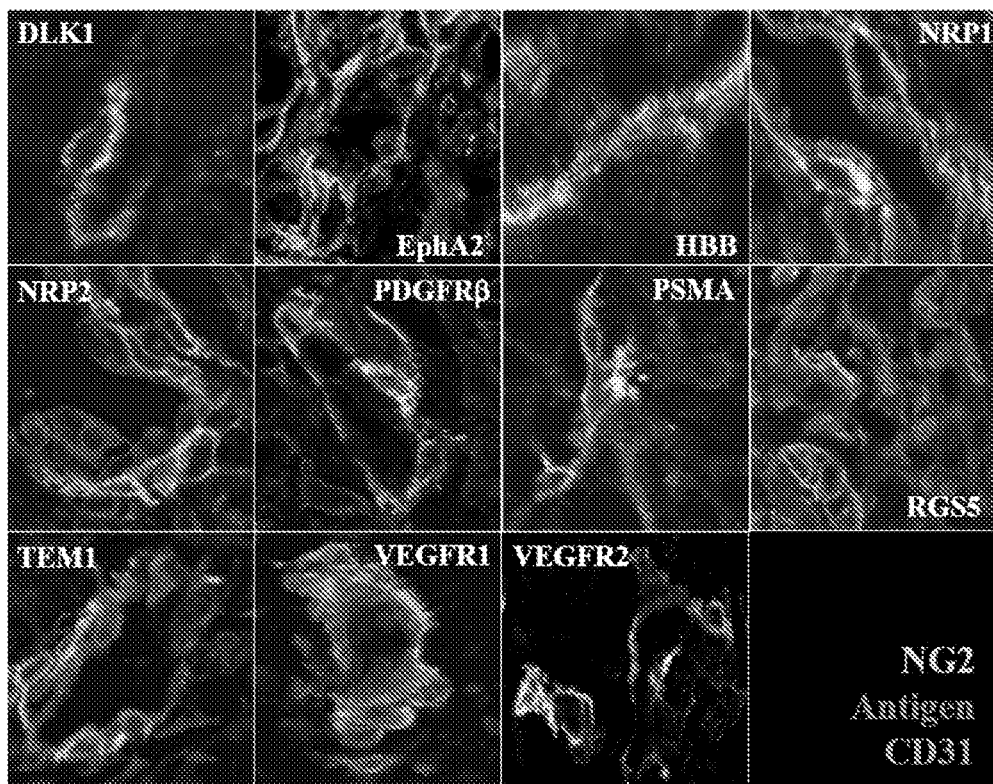


FIG. 15

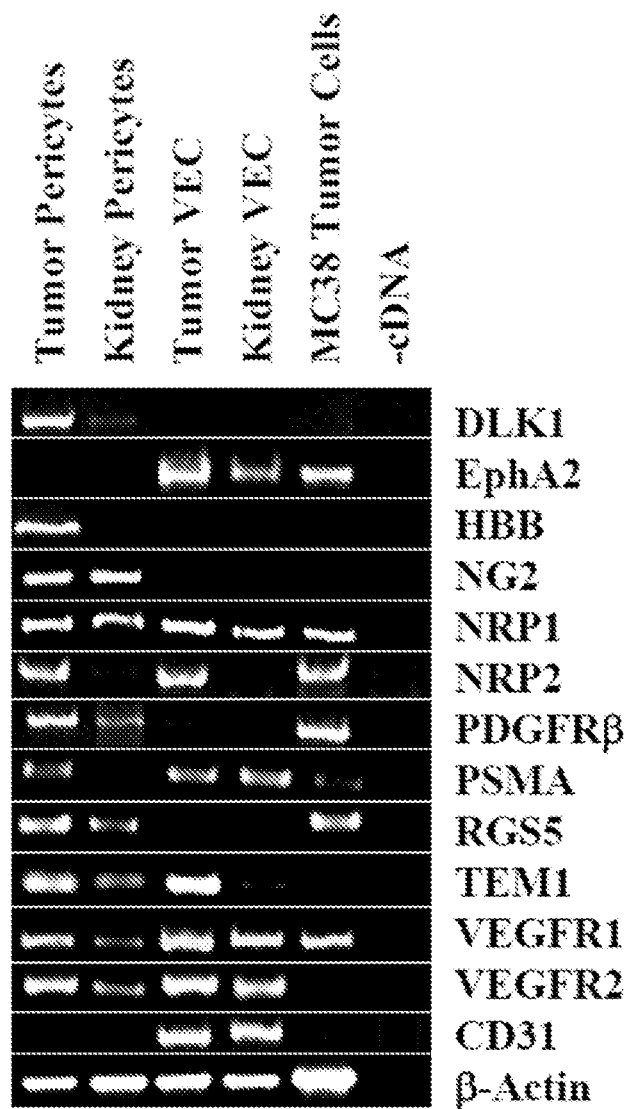


FIG. 16

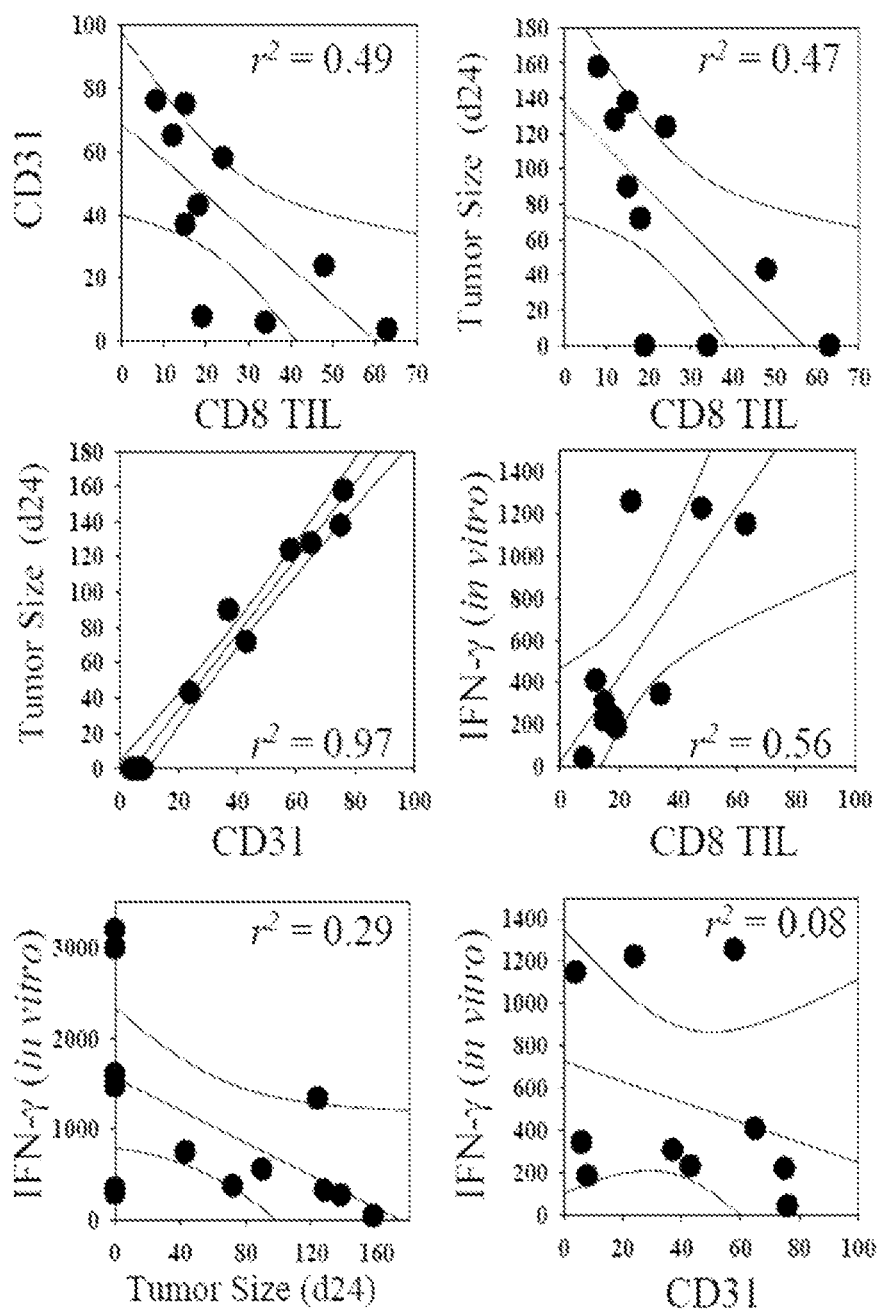


FIG. 17A

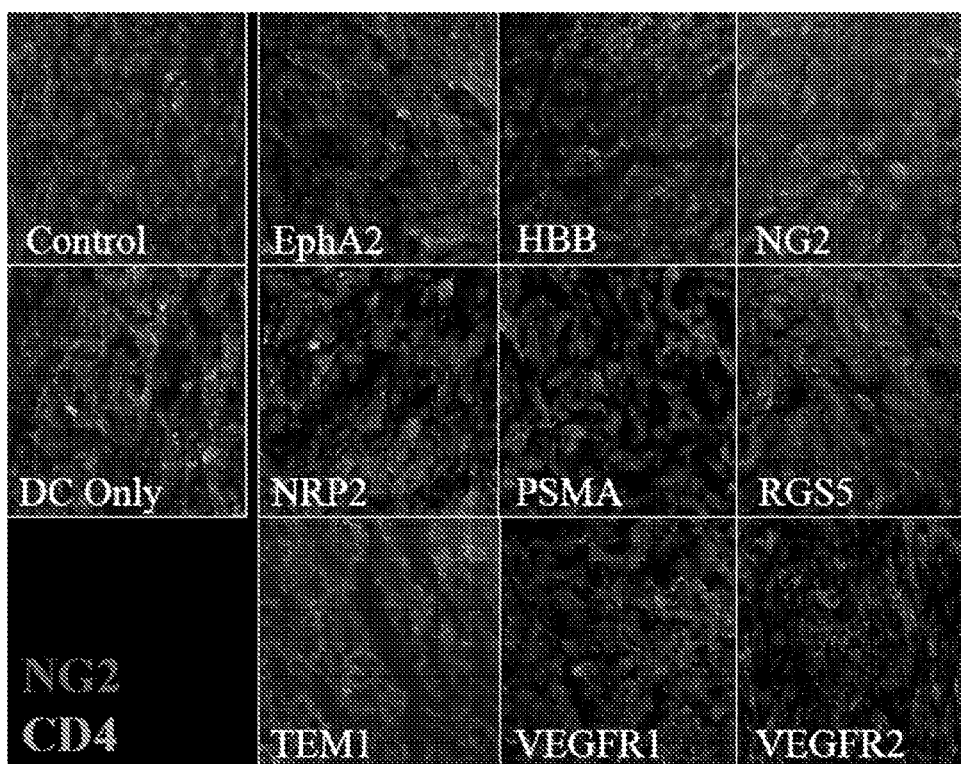


FIG. 17B

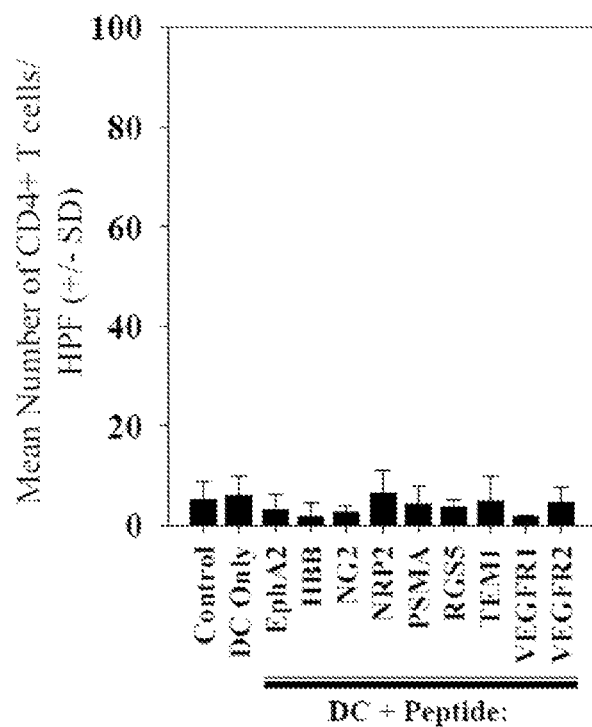


FIG. 18

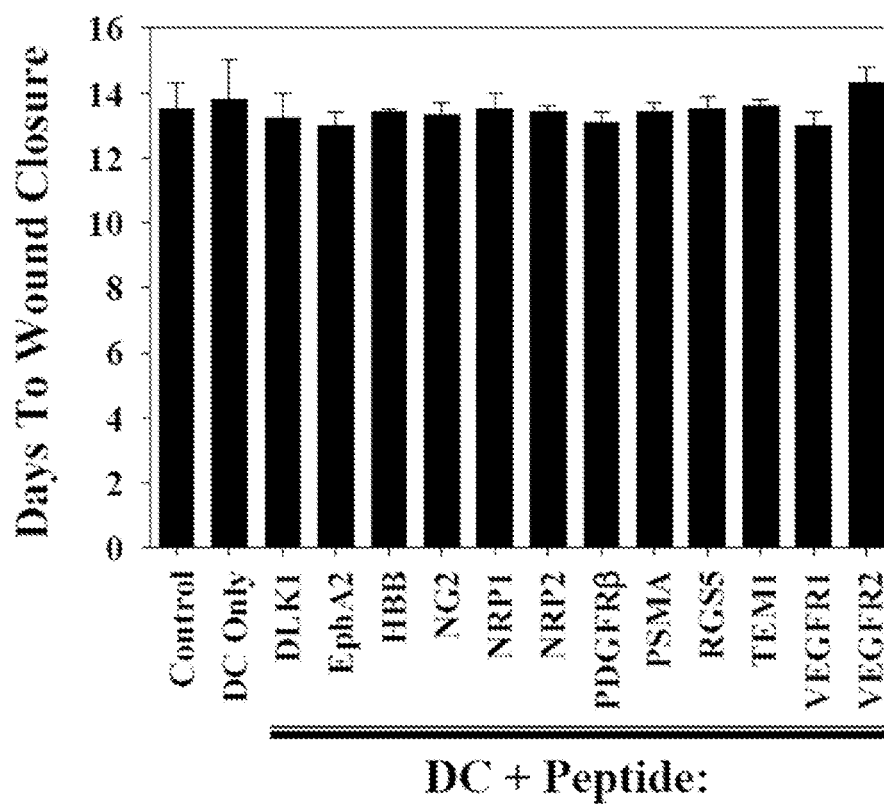


FIG. 19B

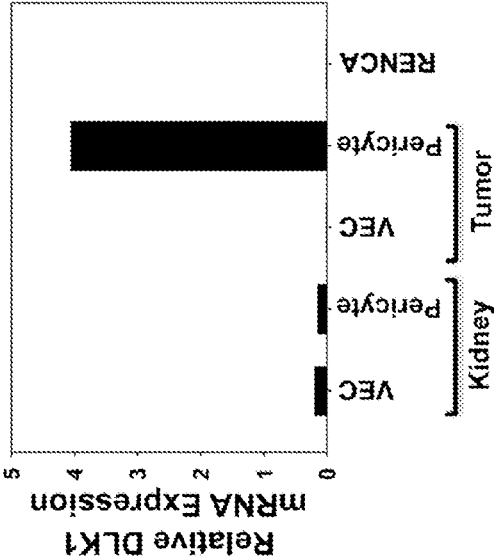


FIG. 19C

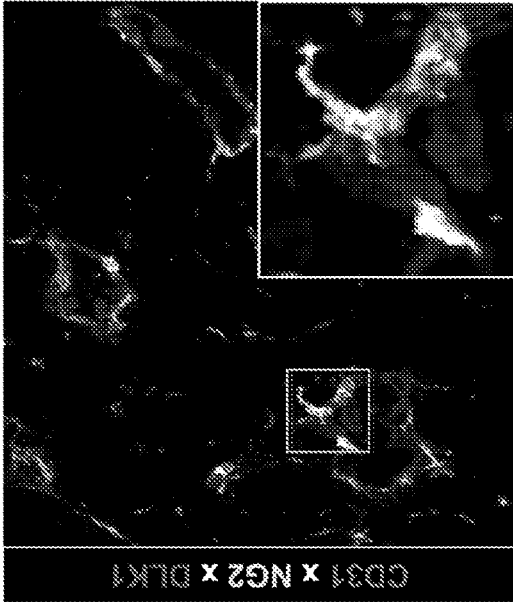
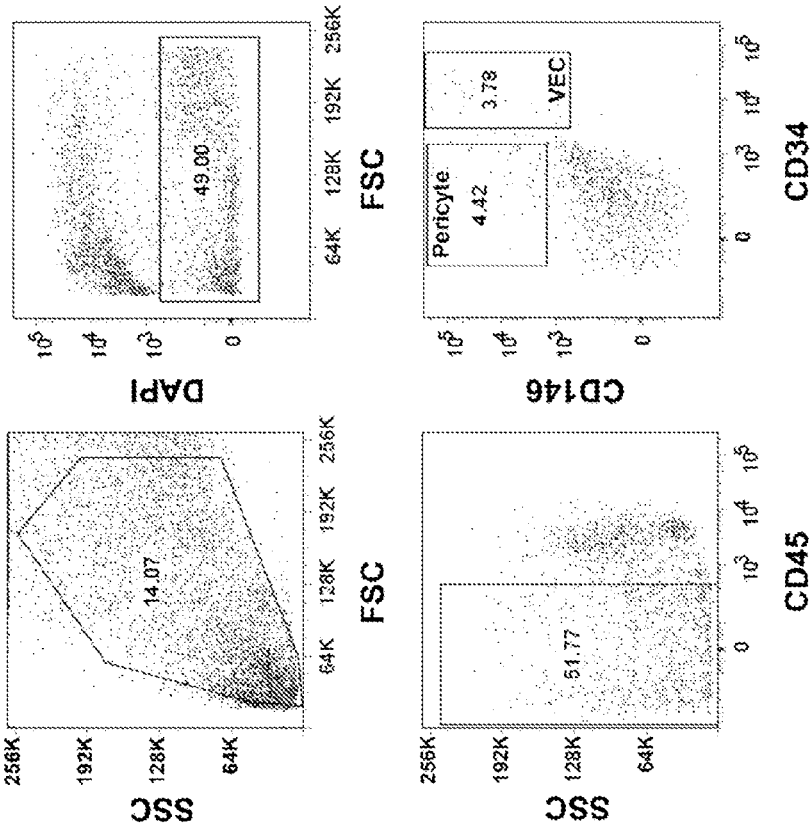
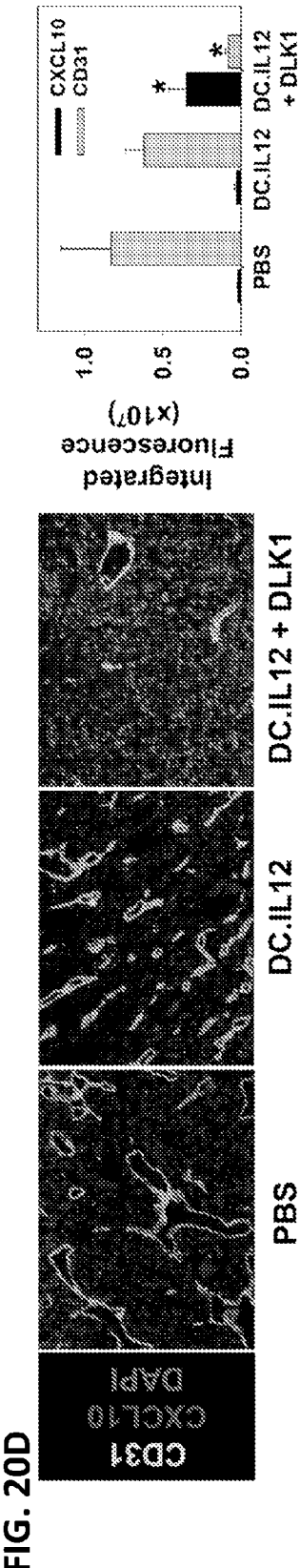
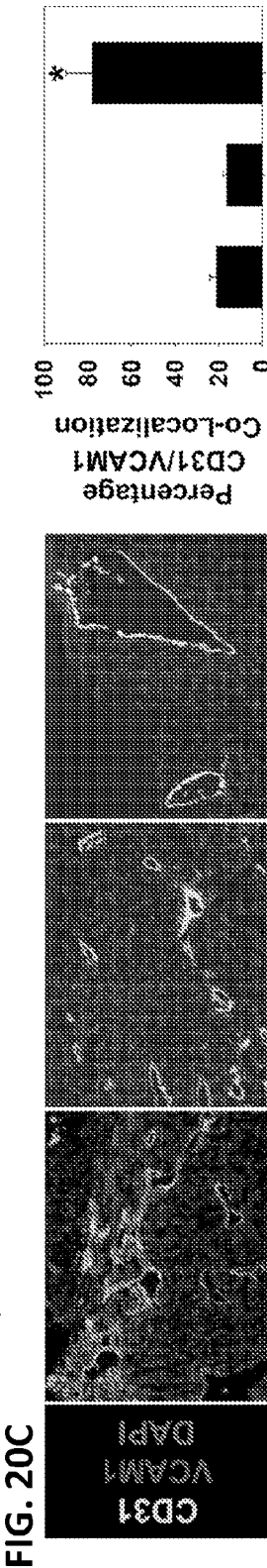
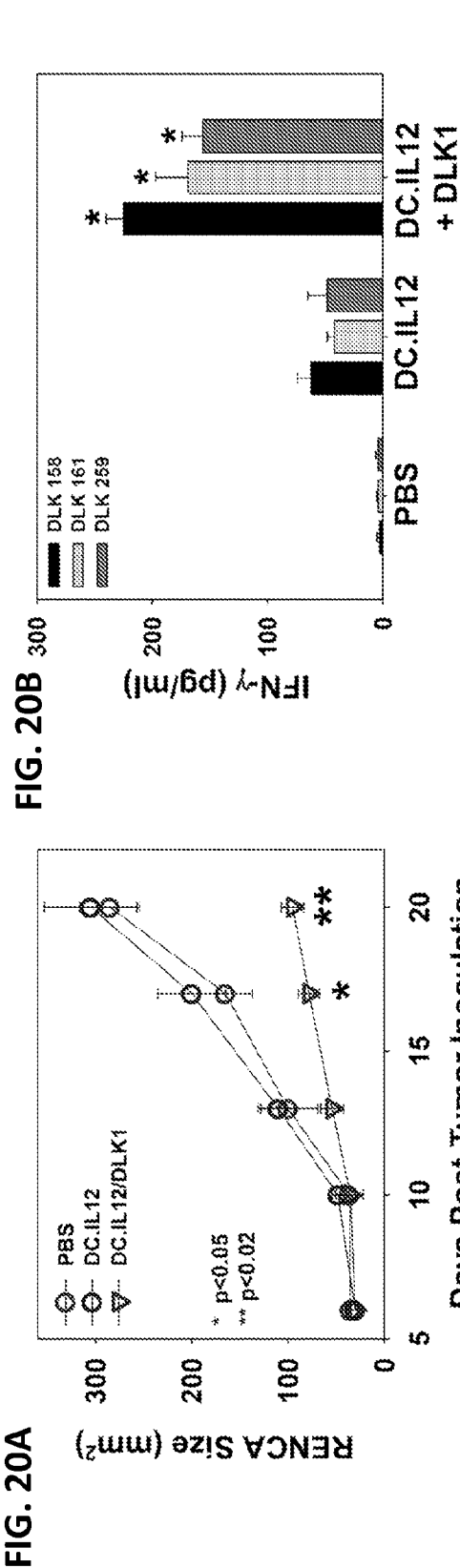


FIG. 19A





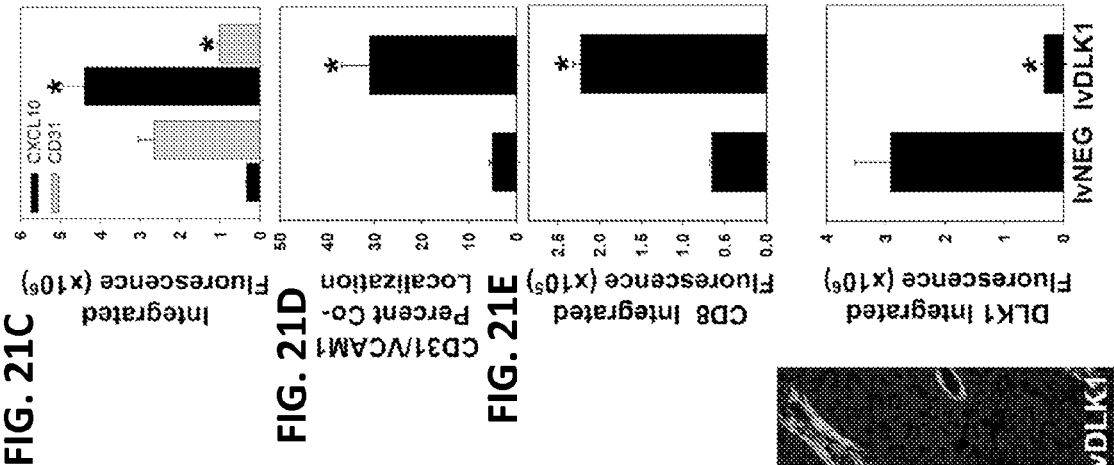


FIG. 21A

FIG. 21B

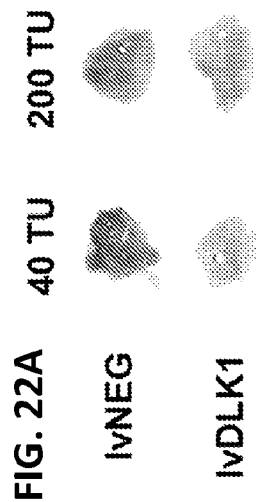


FIG. 22B

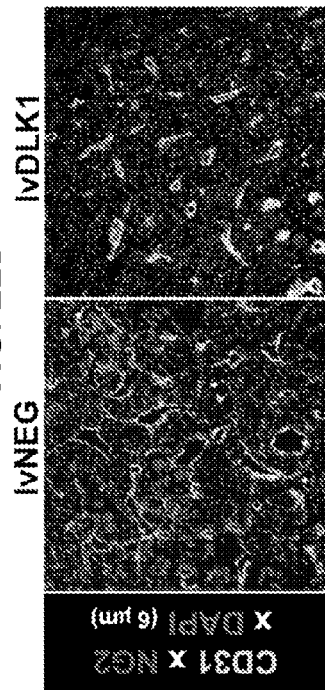


FIG. 22C

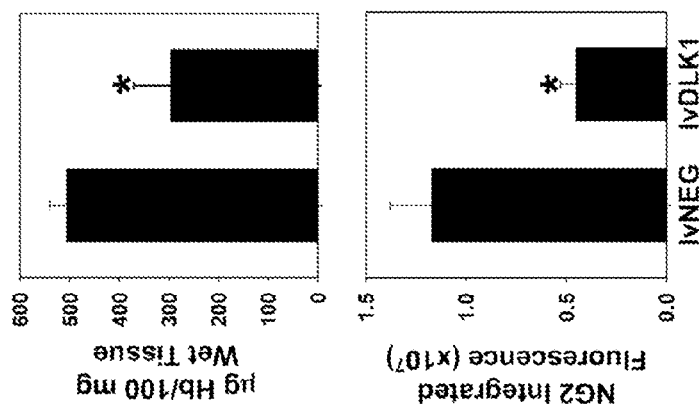
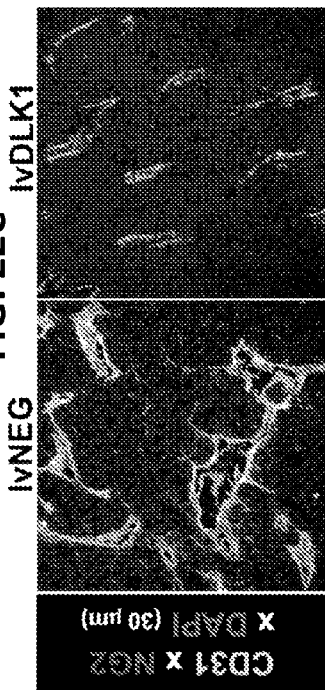


FIG. 22D

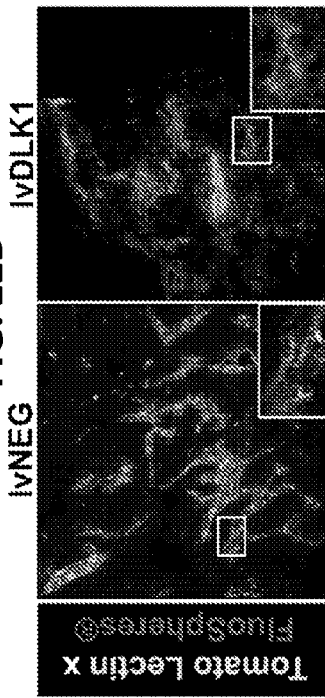
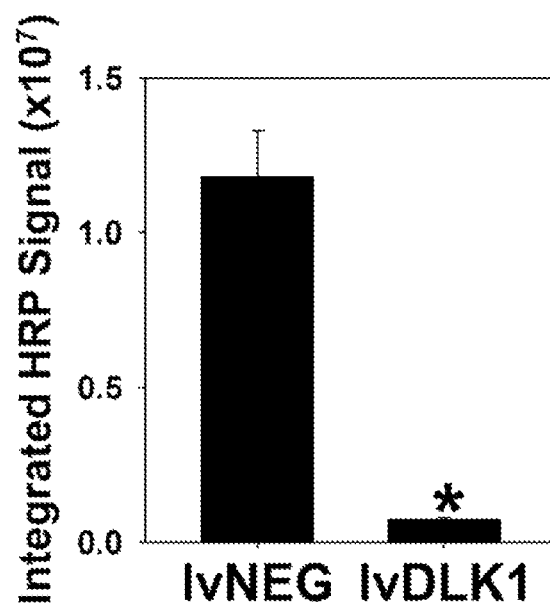
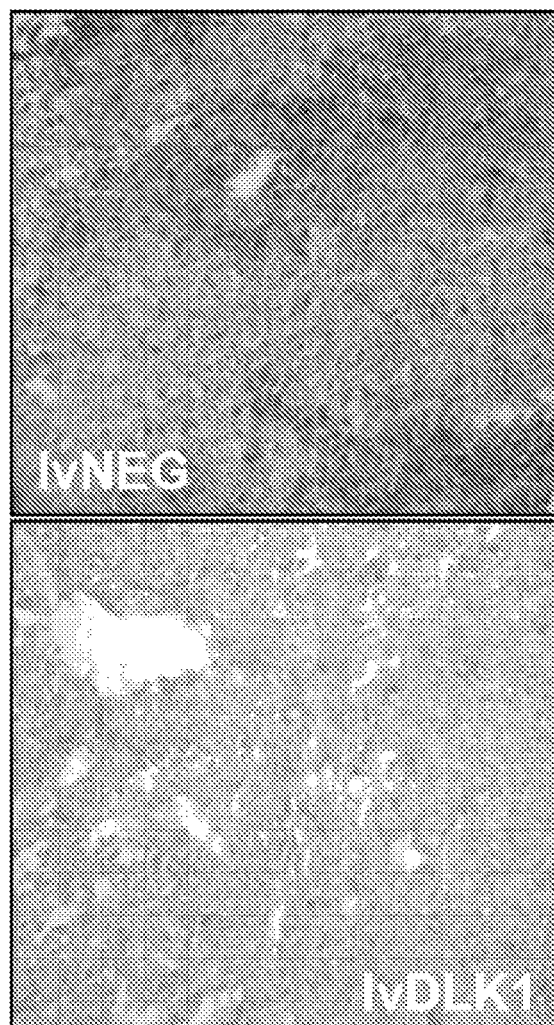


FIG. 23A



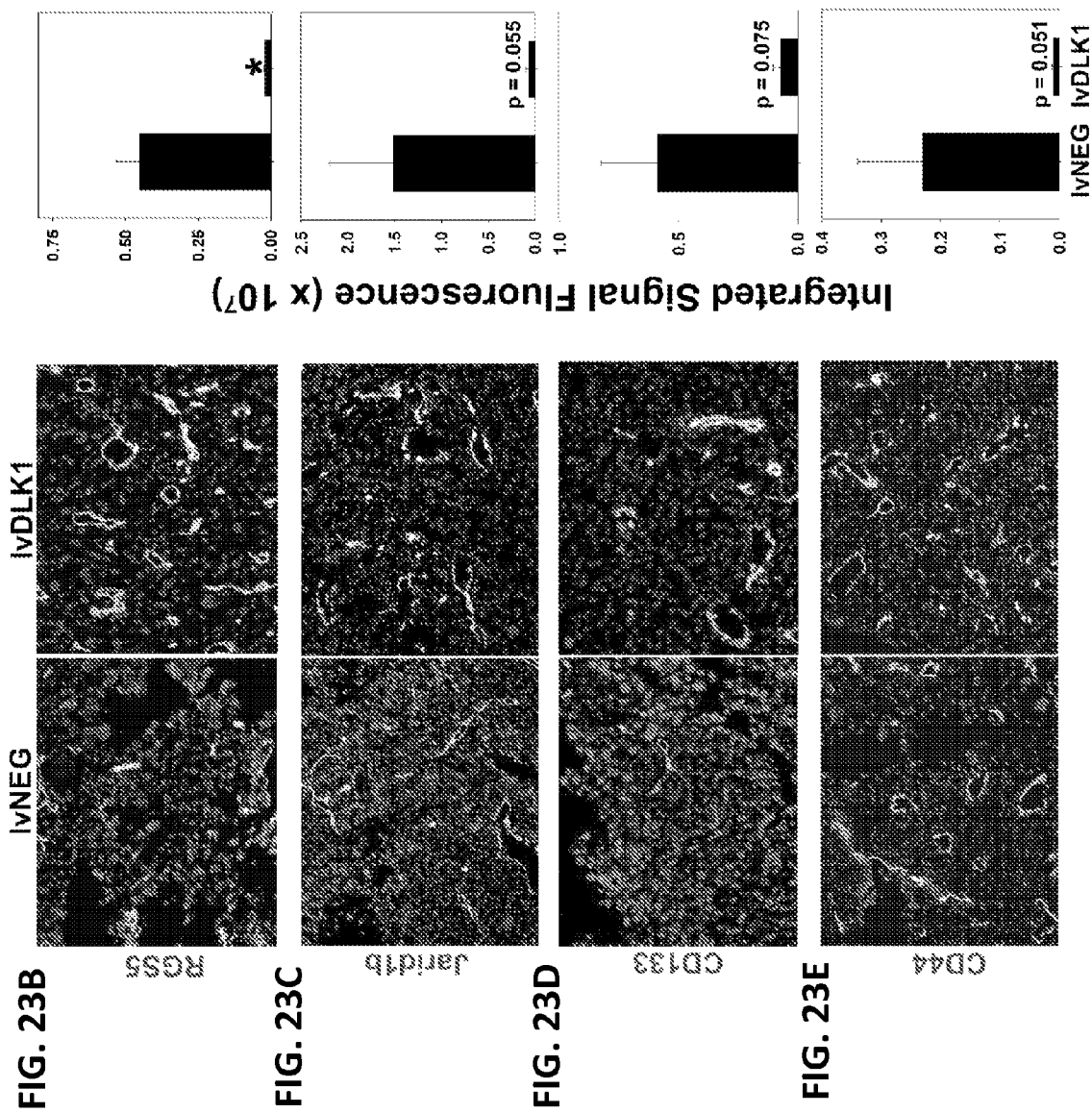
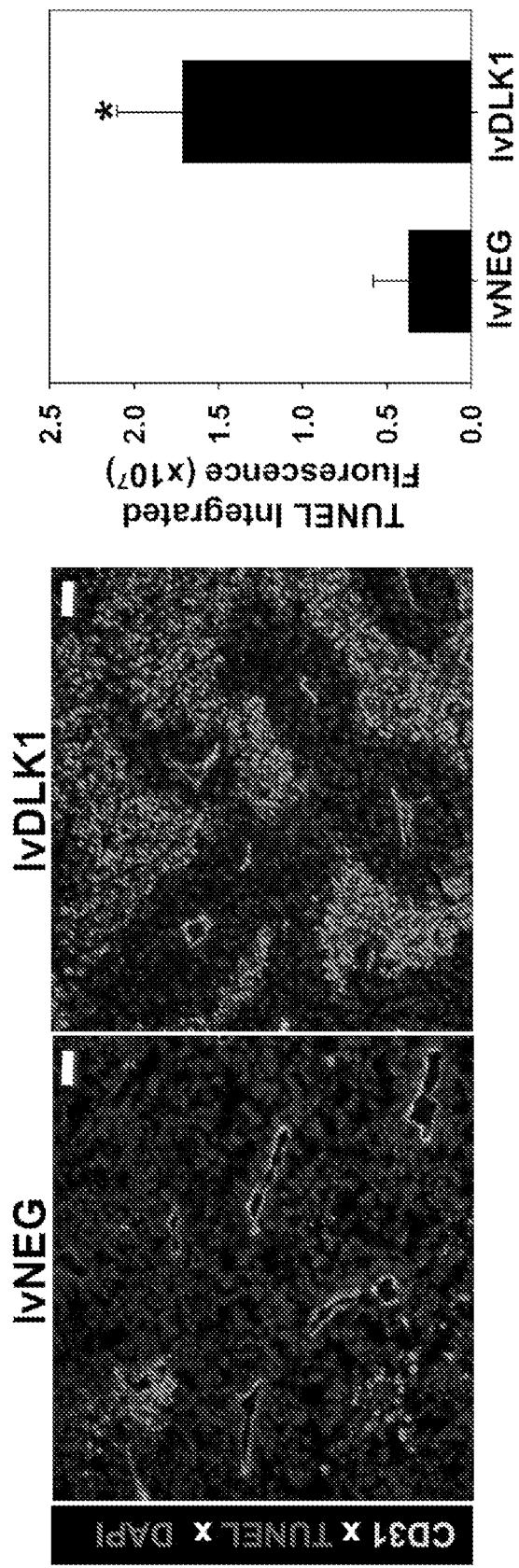


FIG. 24



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IMMUNOGENIC TUMOR ASSOCIATED STROMAL CELL ANTIGEN PEPTIDES AND METHODS OF THEIR USE

This is the U.S. National Stage of International Application No. PCT/US2012/065327, filed Nov. 15, 2012, which was published in English under PCT Article 21(2), which in turn claims the benefit of U.S. Provisional Application No. 61/560,597, filed on Nov. 16, 2011, which is incorporated by reference herein in its entirety.

ACKNOWLEDGMENT OF GOVERNMENT SUPPORT

This invention was made with government support under Grant Nos. R01 NIH CA114071, R01 NIH CA140375 and P50 NIH CA121973 awarded by the National Institutes of Health. The government has certain rights in the invention.

FIELD

This application relates to the field of cancer therapeutics, specifically to molecules such as immunogenic peptides, proteins, and inhibitory nucleic acids for the treatment of cancer.

BACKGROUND

T cell-mediated anti-tumor immunity plays a role in regulating tumor growth, placing selective pressure on the antigenically-heterogeneous cancer cell population throughout disease progression (Ostrand-Rosenberg, *Curr. Opin. Genet. Dev.*, 18: 11-18, 2008; Reiman et al., *Semin. Cancer Biol.*, 17: 275-287, 2007; Bui and Schreiber, *Curr. Opin. Immunol.*, 19: 203-208, 2007). Most tumor-associated antigens (TAAs) recognized by T cells are "self" antigens that may be quantitatively over-expressed by tumor cells of one or more histologic types (Slingluff et al., *Adv. Immunol.*, 90: 243-295, 2006). Clinical trials implementing vaccines and immunotherapies targeting such antigens have exhibited success in promoting increased numbers of specific CD4⁺ and/or CD8⁺ T cell populations in the peripheral blood of patients. There is a need to identify additional tumor associated antigens or combinations of antigens that can be used for cancer immunotherapy.

SUMMARY

Immunogenic tumor associated stromal cell antigen (TASA) peptides are disclosed herein. In some embodiments a plurality of immunogenic TASA peptides is included in a composition. In some embodiments, the immunogenic TASA peptides include at most twelve amino acids from a TASA, such as Protein Delta Homolog 1 (DLK1), Hemoglobin Subunit Beta (HBB), Neuropilin 1 (NRP1), Tumor Endothelial Marker 1 (TEM1), Ephrin Type A Receptor 2 (EphA2), Regulator of G-Protein Signaling 5 (RGS5), or Platelet Derived Growth Factor Receptor β (PDGFR β). In some embodiments, compositions are provided including combinations of these polypeptides. In one non-limiting example, a composition is disclosed including DLK1, HBB, NRP1, and TEM1 peptides. In another non-limiting example, a composition is disclosed including DLK1, HBB, NRP1, TEM1, EphA1 and RGS5 peptides.

In additional embodiments, polynucleotides encoding the immunogenic TASA peptides, vectors including these polynucleotides, host cells transformed with these vectors, and methods of using these peptides, polynucleotides, vectors, and host cells are provided.

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In further embodiments, the immunogenic TASA peptides, polynucleotides, vectors and host cells can be used, for example, for inducing an immune response to one or more TASA or to treat or inhibit cancer.

In additional embodiments, methods are disclosed for treating a tumor, such as by decreasing vascularization of a tumor. The methods include administering to a subject having a tumor an effective amount of a Protein Delta Homolog 1 (DLK1) protein, a nucleic acid encoding the DLK1 protein, or a dendritic cell transformed with the nucleic acid. In some non-limiting examples, the methods also include administering to the subject a therapeutically effective amount of bevacizumab, sunitinib, axitinib, an HSP90 inhibitor, or gencitabine/fludarabine. In additional non-limiting examples, the tumor is a melanoma, hepatocellular carcinoma or colorectal cancer.

BRIEF DESCRIPTION OF THE FIGURES

FIGS. 1A-1B show a series of digital images illustrating that expression of TASA in the established B16 tumor microenvironment (TME). In FIG. 1A, B16 melanoma cells were injected subcutaneously (s.c.) in the right flank of female HHD mice and allowed to establish/progress for 14 days. Animals were then euthanized, with tumors resected, fixed, sectioned and analyzed for expression of the indicated antigens using specific Abs and fluorescence microscopy. Specific antibody against NG2 (green), the indicated antigen of interest (red), and CD31 (blue) were used to distinguish preferential antigen expression in tumor-associated stromal pericytes, vascular endothelial cells (VEC), alternate stromal cells and/or tumor cells. In FIG. 1B, B16 melanoma cells, as well as, flow-sorted (PDGFR β ⁺, CD31^{neg}) pericytes and (PDGFR β ^{neg}, CD31⁺) VEC isolated from day 19 established B16 tumors and tumor-uninvolved kidneys were analyzed for expression of target gene product mRNAs using RT-PCR. All data are reflective of three independent experiments performed for each tumor type.

FIGS. 2A-2C show a series of graphs illustrating that induction of CD8⁺ T cells reactive against TASA after intratumoral delivery of DC.IL12. In FIG. 2A, HLA-A2^{neg} B16 melanoma cells were injected subcutaneously in the right flank of female HLA-A2 Tg (HHD) mice and allowed to establish for seven days. On day seven, mice were randomized into three groups (n=5 mice each) receiving no treatment, intratumoral (i.t.) injection of syngeneic dendritic cells (DC) that were previously infected with recombinant adenovirus encoding mIL-12p70, or DC infected with control (empty) adenovirus (i.e. DC. ψ 5). Animals were retreated using the same therapy on day 14 post-tumor inoculation. In replicate cohorts of animals receiving DC.IL12 therapy, depleting antibodies against CD4 or CD8 were provided beginning on day 6 post-tumor inoculation. Tumor sizes were assessed every 3-4 days and are reported as mean \pm SD in mm². *p<0.05 versus control or DC. ψ 5-treated mice on days \geq 14. In FIG. 2B., on day 19 post-tumor inoculation, the mice were euthanized and CD8⁺ splenocytes isolated by magnetic bead cell sorting (MACS) and cultured with PDGFR β ⁺ CD31^{neg}H-2K^{b(neg)} pericytes or PDGFR β ^{neg}CD31⁺H-2K^{b(neg)} VEC sorted by flow cytometry. After co-culture in the absence or presence of anti-HLA-A2 mAb BB7.2 or anti-MHC class II mAb L243 (10 μ g/well) for 48 h at 37 $^{\circ}$ C., cell-free supernatants were analyzed for mIFN- γ content by specific ELISA. Data are mean \pm SD for triplicate determinations, and are representative of 2 independent experiments performed. *p<0.05 versus kidney cells (pericytes or VEC) and tumor pericytes/VEC in the presence of anti-HLA-A2

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mAb BB7.2. In FIG. 2C, on day 19 post-tumor inoculation, the mice were euthanized and splenocytes and stimulated for five days with stromal peptides. On day five, MACS-isolated CD8⁺ splenocytes were cocultured with HLA-A2⁺ T2 cells loaded with the indicated TASA-derived peptides or HLA-A2^{neg} B16 tumor cells. After a 48 h culture period, cell-free supernatants were analyzed for mIFN- γ concentration by specific ELISA. Data are mean \pm SD for triplicate ELISA determinations. *p<0.05 versus FluM1 control peptide responses. All presented data are representative of 3 independent experiments performed.

FIGS. 3A-3B show a series of scatter plot graphs illustrating that CD8⁺ TIL from DC.IL12-treated mice are enriched in effector cells reactive against tumor pericytes and/or VEC, as well as TASA peptides. B16 tumor-bearing mice were treated as described in FIG. 2. On day 17 post-tumor inoculation, CD8⁺ TIL were isolated from all cohorts of mice, and pericytes and VEC were isolated from the tumors and kidneys of untreated mice. Freshly-sorted CD8⁺ TIL were then co-cultured with pericytes, VEC or T2 cells \pm TASA peptides (1 μ M each of all peptides in Table 4 with the exception of NRP2- or PSMA-derived peptides) for 4-5 hours, before responder CD8⁺ T cells were analyzed for intracellular expression of IFN- γ (FIG. 3A) or cell surface expression of CD107a/b (FIG. 3B) by flow cytometry. Inset numbers reflect the percentage of CD8⁺ T cells expressing intracellular IFN- γ or cell surface CD107a/b. Data are from one representative experiment of two performed.

FIG. 4 shows a series of graphs illustrating the in vitro immunogenicity of TASA-derived peptides in HLA-A2⁺ normal donors and patients with melanoma. The indicated peptides were pulsed onto autologous DC and used to prime and boost CD8⁺ T cells isolated from the peripheral blood of eight normal HLA-A2⁺ donors or ten HLA-A2⁺ patients with melanoma. Seven days after the primary in vitro sensitization (IVS) (melanoma patients) or a secondary IVS boost (normal donors), T cells were analyzed for their reactivity against HLA-A2⁺ T2 cells pulsed with the relevant peptide vs. the negative control HIV-nef₁₉₀₋₁₉₈ peptide. After 24 hours of co-culture, cell-free supernatants were analyzed for levels of secreted IFN- γ using a commercial ELISA. Data are reported in Bar and Whisker plots, with p-values provided for paired pre-versus post-IVS data from normal donors and patients. In addition, p<0.05 was detected for MEL-Post versus ND-Post for the following peptides: DLK1 (309), NG2 (770), NG2 (2238), PDGFR β (891) and RGS5 (5).

FIG. 5 shows a graph illustrating that splenic CD8⁺ T cells from HHD mice effectively treated with DC.IL12 gene therapy develop HLA-A2-restricted responses against melanoma-associated antigens. HHD mice bearing day 7 HLA-A2^{neg} (MART-1⁺, gp100⁺) B16 melanomas were left untreated or they were treated with intratumoral injection of control DC (DC. ψ 5) or DC.IL12 as described in FIG. 2. On day 19 post tumor inoculation (i.e. 5 days after receiving the second injection of DC), CD8⁺ spleen cells were isolated and analyzed for reactivity against the hMART-1₂₆₋₃₅ and hmgp100₂₀₉₋₂₁₇ peptide epitopes presented by the HLA-A2⁺ T2 cell line. After 48 h co-culture of T cells and Ag-loaded T2 cells, cell-free supernatants were harvested and analyzed for IFN- γ content by specific ELISA. *p<0.05 versus T2 only control.

FIG. 6 shows a series of graphs illustrating that TASA-derived peptides bind to HLA-A2 to a variable degree based on the T2 class I stabilization assay. Peptide stabilization of HLA-A2 complexes on the T2 cell line by synthetic peptides was assessed as previously described (Stuber et al., *Eur. J. Immunol.*, 24: 765-768, 1994. FluM1₅₈₋₆₆ (GILGFVFTL)

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was used as a positive HLA-A2 binding control peptide (Tatsumi et al., *Cancer Res.*, 63: 4481-4489, 2003). Overlays of fluorescence histograms are provided for each peptide over a 1-10000 nM dose range, as indicated. Evidence for productive stabilization of HLA-A2 complexes is supported by a shift in staining intensity to the right vs. the no peptide control. Negative control (HLA-A3/A11-binding) HIV-nef₇₃₋₈₂ peptide (Tatsumi et al., *Cancer Res.*, 63: 4481-4489, 2003) failed to promote enhanced HLA-A2 stabilization on T2 cells. Data are from one representative experiment of three independent assays performed.

FIG. 7 shows a set of graphs illustrating that CD8⁺ T cells isolated from B16-bearing HHD mice left untreated or treated with DC. ψ 5 fail to recognize tumor-associated pericytes/VEC. CD8⁺ T cells were MACS-isolated from the spleens of tumor-bearing animals that were left untreated (Control) or that were treated with intratumoral delivered DC. ψ 5, as outlined in FIG. 2B. These T cells were then cultured with flow-sorted tumor- or kidney-derived pericytes or VEC \pm blocking anti-HLA-A2 (BB7.2) or class II (L243) antibodies. Cell-free supernatant was harvested after 24 hours incubation at 37 $^{\circ}$ C. and analyzed using a specific IFN- γ ELISA. Representative data is presented from one of two independent experiments performed.

FIGS. 8A-8C shows a series of graphs illustrating that CD8⁺ TIL isolated from B16-bearing HHD mice treated with DC.IL12 recognize tumor-associated pericytes in an HLA-A2-restricted manner, and fail to recognize HLA-A2^{neg} B16 tumor cells. TIL were isolated from the day 17 melanomas of mice (treated as indicated) and analyzed for reactivity against flow-sorted tumor pericytes as described in FIG. 3 for intracellular IFN- γ or cell surface expression of translocated CD107 using flow cytometry. To assess MHC-restriction in T cell recognition of tumor pericytes, 10 μ g of anti-HLA-A2 mAb BB7.2 or anti-pan class II mAb L243 were added to cultures during the 4-5 hours co-incubation period prior to flow cytometry-based analysis. Inset numbers reflect the percentage of CD8⁺ T cells exhibiting positive response to tumor pericytes or B16 melanoma cells. Data derive from one representative experiment of two independent experiments performed.

FIGS. 9A-9B show a series of graphs illustrating induction of specific/protective CD8⁺ T cells reactive against TASA as a consequence of DC/peptide-based vaccination. In FIG. 9A, HHD mice (five animals/cohort) were vaccinated twice (d-14, d-7) subcutaneously with PBS or with homologous DC.IL12 pulsed with PBS or synthetic peptides (Table 6) derived from the indicated TASA. In cases where more than 1 peptide was identified for a given target antigen, an equimolar pool of the indicated peptides (each 10 μ M) was pulsed onto DC.IL12 and used for vaccination in the relevant cohort. One week after the second immunization, spleens were harvested and splenic CD8⁺ T cells isolated using MACS-beads (Miltenyi). T cells were stimulated in vitro for 48 h using the HLA-A2⁺ T2 cell line pulsed with relevant TASA vs. irrelevant HIV-nef₁₉₀₋₁₉₈ (AFHHVAREL; ref. 24) peptides. Cell-free supernatants were then recovered and IFN- γ levels by ELISA. Data are reported as mean \pm SD for triplicate ELISA determinations, and are representative of 3 independent experiments performed. *p<0.05 vs. HIV-nef control peptide responses. In FIG. 9B, HHD mice were vaccinated twice (days-14 and -7; right flank) subcutaneously with PBS or with homologous DC.IL12 pulsed with PBS or synthetic TASA peptides as indicated in FIG. 1A. In cases where more than 1 peptide is identified for a given target antigen, an equimolar pool of the indicated peptides (each 10 μ M) was pulsed onto DC.IL12 and used for vaccination in the relevant cohort. One

week after the booster vaccine (i.e. day zero), animals were challenged subcutaneously on their left flank with 2×10^6 MC38 colon carcinoma cells. Tumor growth was then monitored every 3-4 days through day 24. All data represent mean tumor area (in mm^2) \pm SD determined from 5 mice/cohort, and are representative of three independent experiments performed. * $p < 0.05$ versus DC only on the indicated days.

FIGS. 10A-10D show a series of digital images and graphs illustrating that MC38 tumors in mice pre-vaccinated with TASA-derived peptides exhibit differential infiltration by CD8^+ T cells and alterations in vascular density. Day 14 MC38 tumors were harvested from HHD mice that had been vaccinated as outlined in FIG. 9B with the indicated peptides (or control PBS or DC:IL12 alone=No peptide). In FIG. 10A., six-micron tissue sections were co-stained with anti- CD8^+ (green) and anti-NG2 (red) antibodies and imaged by fluorescence microscopy. Blue signal=nuclear counterstain using 4',6-diamidino-2-phenylindole (DAPI). FIG. 10B provides a summary of the mean \pm SD number of CD8^+ cells per high-power field (HPF) in MC38 tumors isolated from control or vaccinated mice as depicted in FIG. 10A. In FIG. 10C, tissue sections were co-stained with anti- CD31^+ (green) and anti-NG2 (red) antibodies and imaged by fluorescence microscopy. Blue signal=nuclear counterstain using DAPI. In FIG. 10D, the mean \pm SD number of CD31^+ vessels per HPF of MC38 tumors in control or vaccinated mice are summarized. Representative data is depicted from 1 of 3 independent experiments performed. * $p < 0.05$ versus DC only or untreated control mice.

FIGS. 11A-11C show a series of graphs illustrating that DC:IL12 vaccines containing TASA-derived peptides are therapeutic against MC38 colon carcinomas and B16 melanomas in HHD mice. In FIG. 11A, HHD mice bearing established day seven subcutaneous MC38 tumors (right flank) were left untreated, or they were vaccinated in the left flank with control DC:IL12 or DC:IL12 pulsed with an equimolar pool (10 μM each) of the following TASA-derived peptides: $\text{DLK1}_{326-334}$, $\text{EphA2}_{883-891}$, HBB_{31-39} , $\text{NRP1}_{869-877}$, $\text{FDG-FR}\beta_{890-898}$, RGS5_{5-13} and $\text{TEM1}_{691-700}$. Identical booster vaccines were provided on day 14 post-tumor inoculation. As indicated, two vaccine cohorts were treated with depleting anti- CD4 or anti- CD8 monoclonal antibodies to evaluate the impact of these T cell subsets on therapy outcome. Tumor growth was monitored every 3-4 days through d28. In FIG. 11B, Female HHD or C57BL/6 (B6) mice were inoculated subcutaneously in the right flank with 1×10^5 B16 (HLA-A2^{neg}) tumor cells. After 7 days, animals were randomized into groups of 5 mice exhibiting tumor lesions with a mean surface area of $60-75 \text{ mm}^2$. The mice then received vaccines consisting of isologous control or peptide-pulsed DC:IL12 cells subcutaneously in the left flank on days 10 and 17 (post-tumor inoculation). In cases where more than one peptide was identified for a given target antigen, an equimolar pool of the indicated peptides (each 10 μM) was pulsed onto DC:IL12 and used for vaccination. Tumor size (mean \pm SD) was monitored every 3-4 days through day 34. In FIG. 11A and FIG. 11B, mean tumor area \pm SD is reported for 5 animals/cohort. Data are the representative of those obtained in two independent experiments in each case. * $p < 0.05$ versus DC only on the indicated days. In FIG. 11C, HHD mice bearing subcutaneous B16 melanomas were treated as described in FIG. 11B and followed through day 60 post-tumor inoculation. Data are reported in a Kaplan-Meier plot depicting overall percentage of surviving animals over time. * $p < 0.02$ versus DC only; ** $p < 0.002$ versus DC only (with

refined p-values for differences between treatment cohorts reported in Table 6). Data are cumulative for three independent experiments performed.

FIG. 12 shows a series of graphs illustrating that HHD mice treated for B16 melanoma by treatment with DC:IL12/peptide vaccination exhibit poly-specific anti-TASA Type-1 CD8^+ T (Tc1) responses. HHD mice bearing established day seven B16 melanomas were therapeutically vaccinated with peptides derived from the TASA DLK1 or RGS5 as described in FIG. 11B. Tumors regressed to a non-detectable level over the next two weeks. Sixty days after tumor inoculation, CD8^+ T cells were MACS-isolated from the spleens of these animals and evaluated for IFN- γ production (by ELISA) in response to pericytes and VEC (flow-sorted from day 19 untreated B16 tumors or tumor-uninvolved kidneys of B16-bearing HHD mice), as well as, HLA-A2⁺ T2 cells (control or pulsed with the indicated peptides). * $p < 0.05$ versus anti-class I mAb blockade (when evaluating responses against pericytes, VEC or B16 tumor cells) or T2 cells only (when evaluating anti-peptide responses). Data are reflective of responses observed in three independent experiments.

FIG. 13 shows a series of graphs illustrating that in vivo depletion of CD8^+ , but not CD4^+ , T cells from a cohort of HHD mice effectively treated with TASA peptide-based vaccines results in recurrence of disease at the site of primary tumor inoculation. HHD mice harboring established subcutaneous B16 melanomas received vaccines consisting of syngenic DC:IL12 pulsed with a mixture of TASA peptides on days 7 and 14 (post-tumor inoculation) as outlined in FIG. 11A, resulting in tumor regression in 100% of treated animals. On days 60 and 67 or days 180 and 187 (post-tumor inoculation) mice were depleted of CD4^+ or CD8^+ T cells by intraperitoneal injection with specific antibodies. Control animals received i.p. injections of isotype control antibodies. Specific T cell subset depletions were confirmed by flow cytometry analyses performed on peripheral blood obtained by tail. Animals were then monitored for the reappearance and size of melanomas every 4-7 days. The number of animals evaluated per cohort is indicated within a given panel, with each line representing longitudinal data from a given animal. Data are cumulative from three experiments performed.

FIG. 14. shows a series of digital images illustrating expression of TASA in the established MC38 TME. MC38 colon carcinoma cells were injected subcutaneously in the right flank of female HHD mice and allowed to establish/progress for 14 days. Animals were then euthanized, with tumors resected, fixed, sectioned and analyzed for expression of the indicated antigens using specific antibodies and fluorescence microscopy. Specific antibody against NG2 (green), the indicated antigen of interest (red), and CD31 (blue) were used to distinguish preferential antigen expression in tumor-associated stromal pericytes, VEC, alternate stromal cells and/or tumor cells. Images are reflective of those obtained in three independent experiments performed.

FIG. 15. shows a series of digital images illustrating RT-PCR analysis of "stromal" antigen expression by pericytes, VEC and tumor cells in MC38 tumor-bearing mice. MC38 colon carcinoma cell lines, as well as, flow-sorted tumor- and tumor-uninvolved kidney-associated pericytes and VEC (isolated from HHD mice bearing untreated day 14 tumors) were analyzed for expression of the indicated mRNAs using RT-PCR.

FIG. 16. shows a series of graphs illustrating correlation of biologic parameters assessed in the MC38 tumor model system. Data harvested from FIG. 1 and FIG. 2 were analyzed for the correlation of indicated markers in a pair-wise manner.

Individual data included: CD8+ TIL (day 7 post tumor-inoculation (in mean numbers per HPF), CD31+ vessels in these same lesions (reported a mean number/10 HPF), tumor size (in mm²) on day 24 post-tumor inoculation, and specific production of IFN- γ from splenic CD8+ T cells harvested from control and vaccinated mice on day 14 post-tumor inoculation. Each dot represents a control (DC only) or vaccine cohort evaluated (n=10). For panels including in vitro T cell response data, each symbol reflects cumulative response against a given target antigen (i.e. for DLK1, this represents the summation of responses against each of three peptides, while for RGS5, this reflects response against a single peptide). Note that in all instances, except for the IFN- γ x Tumor Size comparison (n=13), the cohorts vaccinated using DLK1-, NRP1- or PDGFR β -derived peptides are not included in the indicated analysis, as these mice failed to develop lesions capable of being resected for analyses. Linear regression lines are inserted in each panel, with the associated r^2 values reported in each instance. Lines indicating 95% confidence intervals are also provided in each panel.

FIGS. 17A-17B show a series of digital images and a graph illustrating the lack of vaccine-induced impact on CD4+ T cell infiltration into MC38 tumor lesions. In FIG. 17A, tumor sections prepared as described in FIG. 10 were stained using antibodies against CD4 (green) and NG2 (red), then counter-stained using DAPI (blue). The mean number of CD4+ TIL per HPF (+/-SD) was determined over a total of ten fields (FIG. 17B).

FIG. 18 shows a graph illustrating that prior vaccination against TASA does not inhibit wound-healing in HHD mice. Female HHD mice (5 animals/cohort) were vaccinated in the right flank on d-14 and d-7 with saline, 106 DC.IL12 alone or 106 DC.IL12 pulsed with peptides derived from the indicated TASA. In cases where more than one peptide is identified for a given TASA, an equimolar pool of the indicated peptides (each 10 μ M) was pulsed onto DC.IL12 and used for vaccination in the relevant cohort. On d0, mice were anesthetized, with skin on the upper back shaved and sterilized topically, before placement of two 3-mm diameter wounds using a sterilized punch biopsy instrument. Wounds were not treated consequently and no infections were observed in any animals. The time to closure for the 10 wounds/cohort (2 sites/animal x 5 mice/group) were assessed daily and is reported as the mean number of days +/-SD for complete wound closure.

FIGS. 19A-19C show that DLK1 is differentially expressed on RENCA tumor-associated pericytes. RENCA tumor cells were injected subcutaneously (s.c.) into female BALB/c mice and allowed to progress for 21 days after which animals were euthanized and tumors and normal kidneys were removed. In FIG. 19A, tissues were processed into single-cell suspension and sorted by flow cytometry based on forward scatter and side scatter, DAPI exclusion (to exclude dead cells), a CD45^{neg} phenotype, and then selectively into CD146⁺CD34^{neg} pericytes and CD146⁺CD34⁺ VEC populations. In FIG. 19B, mRNA was isolated from sorted pericytes and VEC from normal kidney and RENCA tumor and analyzed for DLK1 expression by real-time PCR. Relative mRNA expression was normalized to housekeeping HPRT1 expression. In FIG. 19C, day 21 RENCA tumor tissue sections were analyzed for expression of CD31, NG2, and DLK1 by fluorescence microscopy. Data are representative of 3 experiments performed.

FIGS. 20A-20D show that DC/DLK1 peptide vaccines are immunogenic and therapeutic in the RENCA model. (FIGS. 20A-20C) BALB/c mice were inoculated with RENCA tumor cells s.c. on the right flank on day 0. In FIG. 20A, After randomizing for similar mean tumor size per treatment cohort

(n=5), mice were injected s.c. on their left flank on days 7 and 14 (post-tumor inoculation) PBS, 10⁶ DC.IL12 or 10⁶ DC.IL12 pre-pulsed with equimolar mix (10 μ M each) of the 3 synthetic DLK1 peptides. Tumor growth (mean \pm SD) was then followed over time. In FIG. 20B, on day 20 post-tumor inoculation, splenic CD8+ T cells were isolated from each cohort and co-cultured with syngenic DC pre-pulsed with individual DLK1 peptides for 24 h, at which time, IFN- γ ELISA were performed on the harvested cell-free supernatants. In FIGS. 20C and 20D, day 20 tumors were fixed, sectioned and analyzed by immunofluorescence microscopy; CD31 (bright grey in FIGS. 20C, 20D), VCAM1 (medium grey in FIG. 20C), CXCL10 (medium grey in FIG. 20D). The percentage of VCAM1 co-localization with CD31 is depicted as a yellow signal in FIG. 20C. Histograms to the right of images reflect mean quantitation (+/-SD) of color pixels from 3 independent fields per slide. Data are representative of 3 independent experiments performed. *p<0.05 versus control treatments (ANOVA).

FIGS. 21A-21E show that Recombinant lentiviral (lv) DLK1-based vaccines are therapeutic and promote a Type-1-polarized TME. (FIGS. 21A-D) BALB/c mice were inoculated s.c. with RENCA tumor cells in the right flank on day 0. (FIG. 21A) After cohort (n=5) randomization for similar mean tumor size on day 10 post-tumor inoculation, mice were treated i.d. in the left flank with 40 TU or 200 TU of lvDLK1 or lvNEG. Tumor size was then monitored longitudinally. In FIGS. 21B, 21C and 21D, on day 27 post-tumor inoculation, mice were euthanized and tumors resected, fixed, sectioned and analyzed by immunofluorescence microscopy for expression of (FIG. 21B) CD31 (bright) and DLK1 (medium grey) with arrows indicating DLK1+ cells, (FIG. 21C) CXCL10 and (FIG. 21D) co-localization of VCAM1 with CD31. In FIG. 21E, CD8+ TIL quantitation is provided. The presented histograms reflect mean quantitation (+/-SD) of color pixels from 3 independent fields per slide. Data are representative of 3 independent experiments performed. *p<0.05 versus control treatments (ANOVA).

FIGS. 22A-22D show that recombinant lvDLK1-based vaccines promote normalization of the tumor vasculature. Mice bearing day 10 RENCA tumors were treated with lvDLK1 or lvNEG as outlined in FIG. 21. On day 27 post-tumor inoculation, mice were euthanized and resected and evaluated macroscopically and for hemoglobin content (FIG. 21A). In FIGS. 21B and 21C, tumor sections were analyzed by immunofluorescence microscopy for expression of CD31 (bright grey) and NG2 (dark grey). In FIG. 21B, 6 μ m sections were imaged by wide-field microscopy, while in FIG. 21C, 30 μ m sections were imaged by confocal microscopy to generate 3D reconstructions. For FIG. 21B, mean data \pm SD of three independent fields per slide is reported for each group from 1 representative experiment of 3 performed. In repeated experiments (FIG. 21D), treated mice received intravenous injections of tomato lectin-FITC to label endothelium (bright grey) and 20 nm FLUORSPHERES[®] to assess vascular permeability (dark grey) on day 24 post-tumor inoculation. Whole tumor tissue was then imaged immediately by confocal microscopy at a depth of 17 μ m. *p<0.05 for lvDLK1 versus lvNEG (t-test).

FIGS. 23A-23E show recombinant lvDLK1-based vaccines promote normoxia in the TME in association with the loss of cells bearing stem cell-like phenotypes. Mice bearing day 10 RENCA tumors were treated with lvDLK1 or lvNEG as outlined in FIG. 21. In FIG. 23A, on day 21, mice were injected i.p. with the hypoxia probe pimonidazole hydrochloride and euthanized, with tumors resected, sectioned, and analyzed by HRP-immunohistochemistry. In FIGS. 21B-

21E, day 21 tumor-bearing mice that did not receive pimonidazole hydrochloride were euthanized, with tumors resected, fixed, sectioned and analyzed by immunofluorescence microscopy for expression of CD31 and RGS5 (FIG. 21B), Jarid1b (FIG. 21C), CD133 (FIG. 21D) and CD44 (FIG. 21E). The presented histograms reflect mean quantitation (+/-SD) of color pixels from 3 independent fields per slide. Data are representative of 3 independent experiments performed. *p<0.05 for lvDLK1 versus lvNEG (t-test).

FIG. 24 shows vascular remodeling after recombinant lvDLK1-based vaccination results in the development of apoptotic "dead zones" in the TME distal to residual blood vessels. Mice bearing day 10 RENCA tumors were treated with lvDLK1 or lvNEG as outlined in FIG. 21. On day 24 post-tumor inoculation, mice were euthanized, with tumors resected, fixed, sectioned and analyzed for expression of CD31 (bright grey) and apoptotic nuclear staining with TUNEL reagent (dark grey). The presented histograms reflect mean quantitation (+/-SD) of color pixels from 3 independent fields per slide. Data are representative of 3 independent experiments performed. *p<0.05 for lvDLK1 versus lvNEG (t-test).

SEQUENCE LISTING

The nucleic and amino acid sequences listed in the accompanying sequence listing are shown using standard letter abbreviations for nucleotide bases, and three letter code for amino acids, as defined in 37 C.F.R. 1.822. Only one strand of each nucleic acid sequence is shown, but the complementary strand is understood as included by any reference to the displayed strand. The Sequence Listing is submitted as an ASCII text file in the form of the file named "Sequence.txt" (106 kb), which was created on Oct. 30, 2015, which is incorporated by reference herein.

In the accompanying sequence listing:

SEQ ID NO: 1 is an exemplary amino acid sequence of an immunogenic DLK1 polypeptide.

SEQ ID NO: 2 is an exemplary amino acid sequence of an immunogenic DLK1 polypeptide.

SEQ ID NO: 3 is an exemplary amino acid sequence of an immunogenic DLK1 polypeptide.

SEQ ID NO: 4 is an exemplary amino acid sequence of an immunogenic HBB polypeptide.

SEQ ID NO: 5 is an exemplary amino acid sequence of an immunogenic HBB polypeptide.

SEQ ID NO: 6 is an exemplary amino acid sequence of an immunogenic NRP1 polypeptide.

SEQ ID NO: 7 is an exemplary amino acid sequence of an immunogenic NRP1 polypeptide.

SEQ ID NO: 8 is an exemplary amino acid sequence of an immunogenic NRP1 polypeptide.

SEQ ID NO: 9 is an exemplary amino acid sequence of an immunogenic TEM1 polypeptide.

SEQ ID NO: 10 is an exemplary amino acid sequence of an immunogenic EphA2 polypeptide.

SEQ ID NO: 11 is an exemplary amino acid sequence of an immunogenic RGS5 polypeptide.

SEQ ID NO: 12 is an exemplary amino acid sequence of an immunogenic PDGFR β polypeptide.

SEQ ID NO: 13 is an exemplary amino acid sequence of an immunogenic NG2 polypeptide.

SEQ ID NO: 14 is an exemplary amino acid sequence of an immunogenic NG2 polypeptide.

SEQ ID NO: 15 is an exemplary amino acid sequence of an immunogenic NRP2 polypeptide.

SEQ ID NO: 16 is an exemplary amino acid sequence of an immunogenic NRP2 polypeptide.

SEQ ID NO: 17 is an exemplary amino acid sequence of an immunogenic NRP2 polypeptide.

SEQ ID NO: 18 is an exemplary amino acid sequence of an immunogenic PSMA polypeptide.

SEQ ID NO: 19 is an exemplary amino acid sequence of an immunogenic VEGFR1 polypeptide.

SEQ ID NO: 20 is an exemplary amino acid sequence of an immunogenic VEGFR2 polypeptide.

SEQ ID NO: 21 is an exemplary amino acid sequence of DLK1.

SEQ ID NO: 22 is an exemplary amino acid sequence of HBB.

SEQ ID NO: 23 is an exemplary amino acid sequence of NRP1.

SEQ ID NO: 24 is an exemplary amino acid sequence of TEM1.

SEQ ID NO: 25 is an exemplary amino acid sequence of EphA2.

SEQ ID NO: 26 is an exemplary amino acid sequence of RGS5.

SEQ ID NO: 27 is an exemplary amino acid sequence of PDGFR β .

SEQ ID NO: 28 is an exemplary amino acid sequence of NG2.

SEQ ID NO: 29 is an exemplary amino acid sequence of NRP2.

SEQ ID NO: 30 is an exemplary amino acid sequence of PSMA.

SEQ ID NO: 31 is an exemplary amino acid sequence of VEGFR1.

SEQ ID NO: 32 is an exemplary amino acid sequence of VEGFR2.

SEQ ID NO: 33-64 are the nucleic acid sequences of primers.

SEQ ID NO: 65 is the amino acid sequence of DLK1₁₅₈₋₁₆₆.

SEQ ID NO: 66 is the amino acid sequence of DLK1₁₆₁₋₁₆₉.

SEQ ID NO: 67 is the amino acid sequence of DLK1₂₅₉₋₂₇₀ and DLK1₂₆₂₋₂₇₀.

SEQ ID NOS: 68-83 are peptide sequences.

SEQ ID NO: 84 is the amino acid sequence of a linker.

DETAILED DESCRIPTION

Terms

Unless otherwise noted, technical terms are used according to conventional usage. Definitions of common terms in molecular biology may be found in Benjamin Lewin, *Genes V*, published by Oxford University Press, 1994 (ISBN 0-19-854287-9); Kendrew et al. (eds.), *The Encyclopedia of Molecular Biology*, published by Blackwell Science Ltd., 1994 (ISBN 0-632-02182-9); and Robert A. Meyers (ed.), *Molecular Biology and Biotechnology: a Comprehensive Desk Reference*, published by VCH Publishers, Inc., 1995 (ISBN 1-56081-569-8).

In order to facilitate review of the various embodiments of this disclosure, the following explanations of specific terms are provided, along with particular examples:

Adjuvant: A vehicle used to enhance antigenicity. Adjuvants include a suspension of minerals (alum, aluminum hydroxide, or phosphate) on which antigen is adsorbed; or water-in-oil emulsion in which antigen solution is emulsified in mineral oil (Freund incomplete adjuvant), sometimes with

the inclusion of killed mycobacteria (Freund's complete adjuvant) to further enhance antigenicity (inhibits degradation of antigen and/or causes influx of macrophages) Immunostimulatory oligonucleotides (such as those including a CpG motif) can also be used as adjuvants (for example see U.S. Pat. No. 6,194,388; U.S. Pat. No. 6,207,646; U.S. Pat. No. 6,214,806; U.S. Pat. No. 6,218,371; U.S. Pat. No. 6,239,116; U.S. Pat. No. 6,339,068; U.S. Pat. No. 6,406,705; and U.S. Pat. No. 6,429,199). Adjuvants include biological molecules (a "biological adjuvant"), such as costimulatory molecules.

Administration: To provide or give a subject an agent, for example, a composition that includes a immunogenic TASA peptide, by any effective route. Exemplary routes of administration include, but are not limited to, oral, injection (such as subcutaneous, intramuscular, intradermal, intraperitoneal, and intravenous) and transdermal (e.g., topical).

Agent: Any substance or any combination of substances that is useful for achieving an end or result; for example, a substance or combination of substances useful for decreasing or reducing a tumor in a subject. In some embodiments, the agent is a chemotherapeutic agent, toxin or anti-angiogenic agent. The skilled artisan will understand that particular agents may be useful to achieve more than one result.

Angiogenesis: A biological process leading to the generation of new blood vessels through sprouting or growth from pre-existing blood vessels. The process involves the migration and proliferation of endothelial cells from preexisting vessels. Angiogenesis occurs during pre- and post-natal development, and in the adult. Angiogenesis occurs during the normal cycle of the female reproductive system, wound healing, and during pathological processes such as cancer, where it is essential for the growth of solid tumors (for review, see Battegay, *J. Molec. Med.*, 73(7): 333-346, 1995; Shchors and Evan, *Cancer Res.*, 67:1630-1633, 2007).

Anti-angiogenic agent: A molecule that decreases or reduces angiogenesis, for example, a molecule that decreases pathological angiogenesis. Additional anti-angiogenic agents include, but are not limited to, vascular endothelial growth factor receptor 2 (VEGFR2) antibodies such as bevacizumab, as well as small molecule tyrosine kinase inhibitors, such as sunitinib. See also, Liu et al., *Seminars in Oncology*, 29(11): 96-103, 2002; Shepherd et al., *Lung Cancer* 34:S81-S89, 2001).

Antigen: A compound, composition, or substance that can stimulate the production of antibodies or a T cell response in an animal, including compositions that are injected or absorbed into an animal. An antigen reacts with the products of specific humoral or cellular immunity, including those induced by heterologous immunogens. The term "antigen" includes all related antigenic epitopes. "Epitope" or "antigenic determinant" refers to a site on an antigen to which B and/or T cells respond. In one embodiment, T cells respond to the epitope, when the epitope is presented in conjunction with an MHC molecule. Epitopes can be formed both from contiguous amino acids or noncontiguous amino acids juxtaposed by tertiary folding of a protein. Epitopes formed from contiguous amino acids are typically retained on exposure to denaturing solvents whereas epitopes formed by tertiary folding are typically lost on treatment with denaturing solvents. An epitope typically includes at least 3, at least 5, at least 9, at least 10, at least 11, at least 12, or about 9-12 amino acids in a unique spatial conformation. Methods of determining spatial conformation of epitopes include, for example, x-ray crystallography and 2-dimensional nuclear magnetic resonance.

An antigen can be a tissue-specific antigen, or a disease-specific antigen. These terms are not exclusive, as a tissue-

specific antigen can also be a disease specific antigen. A tissue-specific antigen is expressed in a limited number of tissues, such as a single tissue. Specific, non-limiting examples of a tissue specific antigen are a prostate specific antigen, a uterine specific antigen, and/or a testes specific antigen. A tissue specific antigen may be expressed by more than one tissue, such as, but not limited to, an antigen that is expressed in more than one reproductive tissue, such as in both prostate and uterine tissue. A disease-specific antigen is expressed coincidentally with a disease process. Specific non-limiting examples of a disease-specific antigen are an antigen whose expression correlates with, or is predictive of, tumor formation, such as prostate cancer and/or uterine cancer and/or testicular cancer. A disease-specific antigen can be an antigen recognized by T cells or B cells.

Cancer, Tumor or Neoplasia: A neoplasm is an abnormal growth of tissue or cells that results from excessive cell division. Neoplastic growth can produce a tumor. The amount of a tumor in an individual is the "tumor burden" which can be measured as the number, volume, or weight of the tumor. A tumor that does not metastasize is referred to as "benign." A tumor that invades the surrounding tissue and/or can metastasize is referred to as "malignant."

Tumors of the same tissue type are primary tumors originating in a particular organ (such as colon or skin). Tumors of the same tissue type may be divided into tumors of different sub-types.

Examples of solid tumors, such as sarcomas (connective tissue cancer) and carcinomas (epithelial cell cancer), include fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, and other sarcomas, synovium, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colorectal carcinoma, lymphoid malignancy, pancreatic cancer, breast cancer, lung cancers, ovarian cancer, prostate cancer, hepatocellular carcinoma, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, medullary thyroid carcinoma, papillary thyroid carcinoma, pheochromocytomas sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, Wilms' tumor, cervical cancer, testicular tumor, seminoma, bladder carcinoma, and CNS tumors (such as a glioma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, melanoma, neuroblastoma and retinoblastoma).

cDNA (complementary DNA): A piece of DNA lacking internal, non-coding segments (introns) and regulatory sequences that determine transcription. cDNA is synthesized in the laboratory by reverse transcription from messenger RNA extracted from cells.

CD4: Cluster of differentiation factor 4, a T cell surface protein that mediates interaction with the MHC Class II molecule. CD4 also serves as the primary receptor site for HIV on T cells during HIV infection. Cells that express CD4 are often helper T cells.

CD8: Cluster of differentiation factor 8, a T cell surface protein that mediates interaction with the MHC Class I molecule. Cells that express CD8 are often cytotoxic T cells.

Chemotherapeutic agent: Any chemical agent with therapeutic usefulness in the treatment of diseases characterized by abnormal cell growth. For example, chemotherapeutic agents are useful for the treatment of cancer, including colorectal and skin cancer. In one embodiment, a chemotherapeutic agent is a radioactive compound. In particular examples, such chemotherapeutic agents are administered in

combination with a treatment that decreases or reduces a tumor or angiogenesis (for example before, during or after administration of a therapeutically effective amount of one or more immunogenic TASA peptides or a composition including a plurality of immunogenic polypeptides). One of skill in the art can readily identify a chemotherapeutic agent of use (see for example, Slapak and Kufe, *Principles of Cancer Therapy*, Chapter 86 in Harrison's Principles of Internal Medicine, 14th edition; Perry et al., *Chemotherapy*, Ch. 17 in Abeloff, Clinical Oncology 2nd ed., © 2000 Churchill Livingstone, Inc; Baltzer, L., Berkery, R. (eds): *Oncology Pocket Guide to Chemotherapy*, 2nd ed. St. Louis, Mosby-Year Book, 1995; Fischer, D. S., Knopf, M. F., Durivage, H. J. (eds): *The Cancer Chemotherapy Handbook*, 4th ed. St. Louis, Mosby-Year Book, 1993; Chabner and Longo, *Cancer Chemotherapy and Biotherapy: Principles and Practice* (4th ed.). Philadelphia: Lippincott Williams & Wilkins, 2005; Skeel, *Handbook of Cancer Chemotherapy* (6th ed.). Lippincott Williams & Wilkins, 2003). Combination chemotherapy is the administration of more than one agent to treat cancer.

Colorectal cancer: A neoplastic tumor of colon, rectum or anus tissue that is or has the potential to be malignant. The main types of colorectal cancer include colorectal carcinomas such as adenocarcinoma and squamous cell carcinoma. Infiltrating (malignant) carcinoma of the colon can be divided into stages (I, II, III and IV). See, e.g., Blake et al. (eds.), *Gastrointestinal Oncology: A practical Guide*, Berlin: Springer-Verlag, 2011.

Consists Of: With regard to a polypeptide, a polypeptide that consists of a specified amino acid sequence does not include any additional amino acid residues, nor does it include additional non-peptide components, such as lipids, sugars or labels.

Conservative variants: "Conservative" amino acid substitutions are those substitutions that do not substantially affect or decrease an activity or antigenicity of an antigenic epitope of DLK1. Specific, non-limiting examples of a conservative substitution include the following examples:

Original Residue	Conservative Substitutions
Al	Ser
Arg	Lys
Asn	Gln, His
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
His	Asn; Gln
Ile	Leu, Val
Leu	Ile; Val
Lys	Arg; Gln; Glu
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

The term conservative variant also includes the use of a substituted amino acid in place of an unsubstituted parent amino acid, provided that antibodies raised to the substituted polypeptide also immunoreact with the unsubstituted polypeptide, and/or that the substituted polypeptide retains the function of the unsubstituted polypeptide. Non-conservative substitutions are those that reduce an activity or antigenicity.

Contacting: Placement in direct physical association, for example solid, liquid or gaseous forms. Contacting includes, for example, direct physical association of fully- and partially-solvated molecules.

Costimulatory molecule: Although engagement of the T-cell receptor with peptide-MHC delivers one signal to the T cell, this signal alone can be insufficient to activate the T cell. Costimulatory molecules are molecules that, when bound to their ligand, deliver a second signal enhancing activation of the T cell. The most well-known costimulatory molecule on the T cell is CD28, which binds to either B7-1 (also called CD80) or B7-2 (also known as CD86). An additional costimulatory molecule is B7-3. Accessory molecules that also provide a second signal for the activation of T cells include intracellular adhesion molecule (ICAM-1 and ICAM-2), leukocyte function associated antigen (LFA-1, LFA-2 and LFA-3). Integrins and tumor necrosis factor (TNF) superfamily members can also serve as co-stimulatory molecules.

Decrease or Reduce: To reduce the quality, amount, or strength of something; for example a reduction in tumor burden. In one example, a therapy reduces a tumor (such as the size of a tumor, the number of tumors, the metastasis of a tumor, or combinations thereof), or one or more symptoms associated with a tumor, for example as compared to the response in the absence of the therapy. In a particular example, a therapy decreases the size of a tumor, the number of tumors, the metastasis of a tumor, or combinations thereof, subsequent to the therapy, such as a decrease of at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90%. Such decreases can be measured using the methods disclosed herein.

Degenerate variant: A polynucleotide encoding an immunogenic TASA peptide that includes a sequence that is degenerate as a result of the genetic code. There are 20 natural amino acids, most of which are specified by more than one codon. Therefore, all degenerate nucleotide sequences are included in this disclosure as long as the amino acid sequence of the immunogenic TASA peptide encoded by the nucleotide sequence is unchanged.

Dendritic cell (DC): Dendritic cells are the principle antigen presenting cells (APCs) involved in primary immune responses. Dendritic cells include plasmacytoid dendritic cells and myeloid dendritic cells. Their major function is to obtain antigen in tissues, migrate to lymphoid organs and present the antigen in order to activate T cells. Immature dendritic cells originate in the bone marrow and reside in the periphery as immature cells.

Effective amount: The amount of an agent (such as an immunogenic TASA peptide or a composition comprising a plurality of immunogenic polypeptides) that alone, or together with one or more additional agents, induces the desired response, such as, for example induction of an immune response to a TASA.

Epitope: An antigenic determinant. These are particular chemical groups or peptide sequences on a molecule that are antigenic (that elicit a specific immune response). An antibody specifically binds a particular antigenic epitope on a polypeptide. Epitopes can be formed both from contiguous amino acids or noncontiguous amino acids juxtaposed by tertiary folding of a protein. Epitopes formed from contiguous amino acids are typically retained on exposure to denaturing solvents whereas epitopes formed by tertiary folding are typically lost on treatment with denaturing solvents. An epitope typically includes at least 3, and more usually, at least 5, about 9, or 8 to 10 amino acids in a unique spatial conformation.

mation. Methods of determining spatial conformation of epitopes include, for example, x-ray crystallography and 2-dimensional nuclear magnetic resonance. See, e.g., "Epitope Mapping Protocols" in *Methods in Molecular Biology*, Vol. 66, Glenn E. Morris, Ed (1996). In one embodiment, an epitope binds an MHC molecule, such an HLA molecule or a DR molecule. These molecules bind polypeptides having the correct anchor amino acids separated by about eight to about ten amino acids, such as nine amino acids.

Host cells: Cells in which a vector can be propagated and its DNA expressed. The cell may be prokaryotic or eukaryotic. The cell can be mammalian, such as a human cell. The term also includes any progeny of the subject host cell. It is understood that all progeny may not be identical to the parental cell since there may be mutations that occur during replication. However, such progeny are included when the term "host cell" is used.

Immune response: A response of a cell of the immune system, such as a B cell, T cell, or monocyte, to a stimulus. In one embodiment, the response is specific for a particular antigen (an "antigen-specific response"). In one embodiment, an immune response is a T cell response, such as a CD4+ response or a CD8+ response. In another embodiment, the response is a B cell response, and results in the production of specific antibodies.

Immunogenic composition: A composition comprising an immunogenic TASA peptide or a plurality of immunogenic TASA peptides, or one or more polynucleotides encoding the immunogenic TASA peptide or plurality of immunogenic TASA peptides that induces a measurable CTL response against cells expressing the corresponding TASA, or induces a measurable B cell response (such as production of antibodies that specifically bind the corresponding TASA) against a TASA peptide. For in vitro use, the immunogenic composition can consist of the isolated nucleic acid, vector including the nucleic acid/or immunogenic peptide. For in vivo use, the immunogenic composition will typically comprise the nucleic acid, vector including the nucleic acid, and/or immunogenic polypeptide, in pharmaceutically acceptable carriers, and/or other agents. An immunogenic composition can optionally include an adjuvant.

Immunogenic TASA peptide: A peptide which comprises an allele-specific motif or other sequence of a tumor associated stromal cell antigen, such that the peptide will bind an MHC molecule and induce a cytotoxic T lymphocyte ("CTL") response, or a B cell response (e.g. antibody production) against the antigen from which the immunogenic peptide is derived.

In one example, an immunogenic TASA peptide is a series of contiguous amino acid residues from a TASA generally between 7 and 20 amino acids in length, such as about 8 to 11 residues in length. Specific immunogenic TASA peptides are disclosed herein that are 9 or 10 amino acid residues in length, or at most 12 amino acids in length, such as 8-15 amino acids in length. Generally, immunogenic TASA peptides can be used to induce an immune response in a subject, such as a B cell response or a T cell response. In one example, an immunogenic TASA peptide, when bound to a Major Histocompatibility Complex Class I molecule, activates cytotoxic T lymphocytes (CTLs) against cells expressing the corresponding wild-type TASA protein. Induction of CTLs using synthetic peptides and CTL cytotoxicity assays known in the art, see U.S. Pat. No. 5,662,907, which is incorporated herein by reference. In one example, an immunogenic peptide includes an allele-specific motif or other sequence such that the peptide will bind an MHC molecule and induce a cytotoxic T

lymphocyte ("CTL") response against the antigen from which the immunogenic peptide is derived.

Isolated: A biological component (such as a nucleic acid, peptide, protein or protein complex) that has been substantially separated, produced apart from, or purified away from other biological components in the cell of the organism in which the component naturally occurs, i.e., other chromosomal and extrachromosomal DNA and RNA, and proteins. Thus, isolated nucleic acids, peptides and proteins include nucleic acids and proteins purified by standard purification methods. The term also embraces nucleic acids, peptides and proteins prepared by recombinant expression in a host cell, as well as, chemically synthesized nucleic acids. A isolated nucleic acid, peptide or protein, for example a polypeptide, can be at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% pure. The epitopes of TASA disclosed herein can be isolated (and/or synthesized) by any means known in the art (see, e.g., *Guide to Protein Purification*, ed. Deutscher, *Meth. Enzymol.* 185, Academic Press, San Diego, 1990; and Scopes, *Protein Purification: Principles and Practice*, Springer Verlag, New York, 1982).

Linker: The terms "conjugating," "joining," "bonding," "labeling" or "linking" refer to making two molecules into one contiguous molecule; for example, linking two polypeptides into one contiguous polypeptide, or covalently attaching an effector molecule or detectable marker radionuclide or other molecule to a polypeptide. The linkage can be either by chemical or recombinant means. "Chemical means" refers to a reaction between the antibody moiety and the effector molecule such that there is a covalent bond formed between the two molecules to form one molecule.

In some embodiments, a linker is an amino acid sequence that covalently links two polypeptide domains. For example, such linkers can be included in the between the immunogenic TASA epitopes disclosed herein to provide rotational freedom to the linked polypeptide domains and thereby to promote proper domain folding and presentation to a MHC. By way of example, in a recombinant polypeptide comprising two immunogenic TASA peptide domains, linker sequences can be provided between them, such as a polypeptide comprising immunogenic TASA peptide-linker-immunogenic TASA peptide. Linker sequences, which are generally between 2 and 25 amino acids in length, are well known in the art and include, but are not limited to, the glycine(4)-serine spacer (GGGGS (SEQ ID NO: 84)×3) described by Chaudhary et al., *Nature* 339:394-397, 1989.

Lymphocytes: A type of white blood cell that is involved in the immune defenses of the body. There are two main types of lymphocytes: B cells and T cells.

Major Histocompatibility Complex (MHC): A generic designation meant to encompass the histocompatibility antigen systems described in different species, including the human leukocyte antigens ("HLA").

Open reading frame (ORF): A series of nucleotide triplets (codons) coding for amino acids without any internal termination codons. These sequences are usually translatable into a peptide.

Operably linked: A first nucleic acid sequence is operably linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence, such as a sequence that encodes an immunogenic TASA peptide. Generally, operably linked DNA sequences are con-

tiguous and, where necessary to join two protein-coding regions, in the same reading frame.

Pathological angiogenesis: Angiogenesis that is medically undesired or harmful to a subject, such as angiogenesis associated with a tumor or the generation of blood vessels in or surrounding a tumor. Other examples of pathological angiogenesis include corneal or retinal angiogenesis (as in a corneal transplant or the retina of a subject with macular degeneration or diabetes).

Peptide Modifications: Immunogenic TASA peptides include synthetic embodiments of peptides described herein. In addition, analogs (non-peptide organic molecules), derivatives (chemically functionalized peptide molecules obtained starting with the disclosed peptide sequences) and variants (homologs) of these peptides can be utilized in the methods described herein. Each peptide of this disclosure is comprised of a sequence of amino acids, which may be either L- and/or D-amino acids, naturally occurring and otherwise.

Peptides can be modified by a variety of chemical techniques to produce derivatives having essentially the same activity as the unmodified peptides, and optionally having other desirable properties. For example, carboxylic acid groups of the protein, whether carboxyl-terminal or side chain, can be provided in the form of a salt of a pharmaceutically-acceptable cation or esterified to form a C₁-C₁₆ ester, or converted to an amide of formula NR₁R₂ wherein R₁ and R₂ are each independently H or C₁-C₁₆ alkyl, or combined to form a heterocyclic ring, such as a 5- or 6-membered ring. Amino groups of the peptide, whether amino-terminal or side chain, can be in the form of a pharmaceutically-acceptable acid addition salt, such as the HCl, HBr, acetic, benzoic, toluene sulfonic, maleic, tartaric and other organic salts, or can be modified to C₁-C₁₆ alkyl or dialkyl amino or further converted to an amide.

Hydroxyl groups of the peptide side chains may be converted to C₁-C₁₆ alkoxy or to a C₁-C₁₆ ester using well-recognized techniques. Phenyl and phenolic rings of the peptide side chains may be substituted with one or more halogen atoms, such as fluorine, chlorine, bromine or iodine, or with C₁-C₁₆ alkyl, C₁-C₁₆ alkoxy, carboxylic acids and esters thereof, or amides of such carboxylic acids. Methylene groups of the peptide side chains can be extended to homologous C₂-C₄ alkenes. Thiols can be protected with any one of a number of well-recognized protecting groups, such as acetamide groups. Those skilled in the art will also recognize methods for introducing cyclic structures into the peptides of this invention to select and provide conformational constraints to the structure that result in enhanced stability.

Peptidomimetic and organomimetic embodiments are envisioned, whereby the three-dimensional arrangement of the chemical constituents of such peptido- and organomimetics mimic the three-dimensional arrangement of the peptide backbone and component amino acid side chains, resulting in such peptido- and organomimetics of an immunogenic TASA peptide having measurable or enhanced ability to generate an immune response. For computer modeling applications, a pharmacophore is an idealized three-dimensional definition of the structural requirements for biological activity. Peptido- and organomimetics can be designed to fit each pharmacophore with current computer modeling software (using computer assisted drug design or CADD). See Walters, "Computer-Assisted Modeling of Drugs," in Klegerman & Groves, eds., 1993, *Pharmaceutical Biotechnology*, Interpharm Press: Buffalo Grove, Ill., pp. 165-174 and *Principles of Pharmacology*, Munson (ed.) 1995, Ch. 102, for descriptions of techniques used in CADD. Also included are mimetics prepared using such techniques.

Pharmaceutically acceptable carriers: The pharmaceutically acceptable carriers provided herein are conventional. *Remington's Pharmaceutical Sciences*, by E. W. Martin, Mack Publishing Co., Easton, Pa., 15th Edition (1975), describes compositions and formulations suitable for pharmaceutical delivery of the fusion proteins herein disclosed.

In general, the nature of the carrier will depend on the particular mode of administration being employed. For instance, parenteral formulations usually include injectable fluids that include pharmaceutically and physiologically acceptable fluids such as water, physiological saline, balanced salt solutions, aqueous dextrose, glycerol or the like as a vehicle. For solid compositions (e.g., powder, pill, tablet, or capsule forms), conventional non-toxic solid carriers can include, for example, pharmaceutical grades of mannitol, lactose, starch, or magnesium stearate. In addition to biologically-neutral carriers, pharmaceutical compositions to be administered can contain minor amounts of non-toxic auxiliary substances, such as wetting or emulsifying agents, preservatives, and pH buffering agents and the like, for example sodium acetate or sorbitan monolaurate.

Polynucleotide: The term polynucleotide or nucleic acid sequence refers to a polymeric form of nucleotide at least 10 bases in length. A recombinant polynucleotide includes a polynucleotide that is not immediately contiguous with both of the coding sequences with which it is immediately contiguous (one on the 5' end and one on the 3' end) in the naturally occurring genome of the organism from which it is derived. The term therefore includes, for example, a recombinant DNA which is incorporated into a vector; into an autonomously replicating plasmid or virus; or into the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (e.g., a cDNA) independent of other sequences. The nucleotides can be ribonucleotides, deoxyribonucleotides, or modified forms of either nucleotide. The term includes single- and double-stranded forms of DNA.

Polypeptide or Peptide: A polymer in which the monomers are amino acid residues that are joined together through amide bonds. The amino acids included in a polypeptide may be subject to post-translational modification (e.g., glycosylation or phosphorylation). A polypeptide or peptide can be between 3 and 30 amino acids in length. In one embodiment, a polypeptide or peptide is from 8 to 12 amino acids in length. In several embodiments, a polypeptide or peptide is at most 12 amino acids in length, for example, 9, 10, 11 or 12 amino acids in length. In some embodiments, a protein is at least 100 amino acids in length, for example, at least 150, at least 200, at least 250, at least 300, at least 350, at least 400, at least 450, or at least 500 amino acids in length.

Plurality: Two or more of a molecule, such as 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or more of a molecule.

Promoter: An array of nucleic acid control sequences which direct transcription of a nucleic acid. A promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. In one embodiment, a promoter includes an enhancer. In another embodiment, a promoter includes a repressor element. In these embodiments, a chimeric promoter is created (a promoter/enhancer chimera or a promoter/repressor chimera, respectively). Enhancer and repressor elements can be located adjacent to, or distal to the promoter, and can be located as much as several thousand base pairs from the start site of transcription. Examples of promoters include, but are not limited to the SV40 promoter, the CMV enhancer-promoter, and the CMV enhancer/ β -actin promoter. Both constitutive and inducible promoters are included (see e.g., Bitter et al., *Methods in Enzymology* 153:

516-544, 1987). Also included are those promoter elements which are sufficient to render promoter-dependent gene expression controllable for cell-type specific, tissue-specific, or inducible by external signals or agents; such elements may be located in the 5' or 3' regions of the gene. Promoters produced by recombinant DNA or synthetic techniques can also be used to provide for transcription of the nucleic acid sequences.

Recombinant: A recombinant nucleic acid is one that has a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques.

Sequence identity: The similarity between amino acid sequences is expressed in terms of the similarity between the sequences, otherwise referred to as sequence identity. Sequence identity is frequently measured in terms of percentage identity (or similarity or homology); the higher the percentage, the more similar the two sequences are. Homologs or variants of an immunogenic TASA peptide or DLK1 will possess a relatively high degree of sequence identity when aligned using standard methods.

Methods of alignment of sequences for comparison are well known in the art. Various programs and alignment algorithms are described in: Smith and Waterman, *Adv. Appl. Math.* 2:482, 1981; Needleman and Wunsch, *J. Mol. Biol.* 48:443, 1970; Higgins and Sharp, *Gene* 73:237, 1988; Higgins and Sharp, *CABIOS* 5:151, 1989; Corpet et al., *Nucleic Acids Research* 16:10881, 1988; and Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444, 1988. Altschul et al., *Nature Genet.* 6:119, 1994, presents a detailed consideration of sequence alignment methods and homology calculations.

The NCBI Basic Local Alignment Search Tool (BLAST) (Altschul et al., *J. Mol. Biol.* 215:403, 1990) is available from several sources, including the National Center for Biotechnology Information (NCBI, Bethesda, Md.) and on the internet, for use in connection with the sequence analysis programs blastp, blastn, blastx, tblastn and tblastx. A description of how to determine sequence identity using this program is available on the NCBI website on the internet.

Homologs and variants of an immunogenic TASA peptide or DLK1 are typically characterized by possession of at least 75%, for example at least 80%, sequence identity counted over the full length alignment with the amino acid sequence of the immunogenic TASA peptide using the NCBI Blast 2.0, gapped blastp set to default parameters. For comparisons of amino acid sequences of greater than about 30 amino acids, the Blast 2 sequences function is employed using the default BLOSUM62 matrix set to default parameters, (gap existence cost of 11, and a per residue gap cost of 1). When aligning short peptides (fewer than around 30 amino acids), the alignment should be performed using the Blast 2 sequences function, employing the PAM30 matrix set to default parameters (open gap 9, extension gap 1 penalties). Proteins with even greater similarity to the reference sequences will show increasing percentage identities when assessed by this method, such as at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, or at least 99% sequence identity. When less than the entire sequence is being compared for sequence identity, homologs and variants will typically possess at least 80% sequence identity over short windows of 10-20 amino acids, and can possess sequence identities of at least 85% or at least 90% or 95% depending on their similarity to the reference sequence. Methods for determining sequence identity over such short windows are available at the

NCBI website on the internet. One of skill in the art will appreciate that these sequence identity ranges are provided for guidance only; it is entirely possible that strongly significant homologs could be obtained that fall outside of the ranges provided.

Skin cancer: A neoplastic tumor of skin tissue that is or has the potential to be malignant. Melanoma is a skin cancer of transformed melanocytes (cells that make the pigment melanin). Melanocytes are found primary in the skin, but are also present in the bowel and eye. Melanoma in the skin includes superficial spreading melanoma, nodular melanoma, acral lentiginous melanoma, and lentigo maligna (melanoma). Any of the above types may produce melanin or can be amelanotic. Similarly, any subtype may show desmoplasia (dense fibrous reaction with neurotropism), which is a marker of aggressive behavior and a tendency for local recurrence. Other melanomas include clear cell sarcoma, mucosal melanoma and uveal melanoma. Melanoma is staged from I to IV. See, e.g., Thompson et al. (eds), *Textbook of Melanoma: Pathology, Diagnosis and Management*, London: Taylor & Francis, 2004.

Stromal cells: Cells forming the connective tissue of any organ. Examples of stromal cells include fibroblasts (such as myofibroblasts), leukocytes, pericytes (such as vascular pericytes) and endothelial cells (such as vascular endothelial cells).

Subject: Any mammal, such as humans, non-human primates, pigs, sheep, cows, rodents and the like. In two non-limiting examples, a subject is a human subject or a murine subject. Thus, the term "subject" includes both human and veterinary subjects.

T Cell: A white blood cell critical to the immune response. T cells include, but are not limited to, CD4⁺ T cells and CD8⁺ T cells. A CD4⁺ T lymphocyte is an immune cell that carries a marker on its surface known as "cluster of differentiation 4" (CD4). These cells, also known as helper T cells, help orchestrate the immune response, including antibody responses as well as killer T cell responses. CD8⁺ T cells carry the "cluster of differentiation 8" (CD8) marker. In one embodiment, a CD8 T cell is a cytotoxic T lymphocyte. In another embodiment, a CD8 cell is a suppressor T cell.

Tumor Associated Microenvironment (TME): A tumor and the area immediately surrounding a tumor, including, for example, blood vessels intersecting or contacting the tumor.

Tumor Associated Stromal Cell: A stromal cell included in a tumor or the tumor microenvironment. For example, vascular endothelial cells (VECs) and pericytes included in blood vessels intersecting or contacting tumor.

Tumor Associated Stromal Cell Antigen (TASA): An antigenic molecule expressed by a tumor associated stromal cell. Examples of TASA include Protein Delta Homolog 1 (DLK1; SEQ ID NO: 21), Hemoglobin Subunit Beta (HBB; SEQ ID NO: 22), Neuropilin 1 (NRP1; SEQ ID NO: 23), Tumor Endothelial Marker 1 (TEM1; SEQ ID NO: 24), Ephrin Type A Receptor 2 (EphA2; SEQ ID NO: 25), Regulator of G-Protein Signaling 5 (RGS5; SEQ ID NO: 26), Platelet Derived Growth Factor Receptor β (PDGFR β ; SEQ ID NO: 27), melanoma chondroitin sulfate proteoglycan (NG2; SEQ ID NO: 28), Neuropilin 2 (NRP2; SEQ ID NO: 29), Glutamate Carboxypeptidase 2, (PSMA; SEQ ID NO: 30), Vascular Endothelial Growth Factor 1 (VEGFR1; SEQ ID NO: 31), Vascular Endothelial Growth Factor Receptor 2 (VEGFR2; SEQ ID NO: 32). (See, e.g., Komita et al., *Cancer Res.*, 68: 8076-8084, 2008; Hatano et al., *J. Transl. Med.*, 2: 40, 2004; Maciag et al., *Cancer Res.*, 68: 8066-8075, 2008; Ishizaki et al., *Clin. Cancer Res.*, 12: 5841-5849, 2006; Wada et al., *Cancer Res.*, 65: 4939-4946, 2005; Kaplan et al., *Vaccine*, 24:

6994-7002, 2006; Liu et al., *Cytokine*, 32: 206-212, 2005; Silver et al., *Clin. Cancer Res.*, 3: 81-85, 1997; Harada et al., *Oncol. Rep.*, 12: 601-607, 2004; Bondjers et al., *Am. J. Pathol.*, 162: 721-729, 2003; Boss et al., *Clin. Cancer Res.*, 13: 3347-3355, 2007; Christian et al., *Am. J. Pathol.*, 172: 486-494, 2008. Several embodiments include an immunogenic peptide from a TASA. In some embodiments, a plurality of immunogenic peptides from one or more TASA is provided in a composition.

Tumor burden: The total volume, number, metastasis, or combinations thereof of tumor or tumors in a subject.

Therapeutically effective amount: The amount of an agent (such as immunogenic TASA peptide, a DLK1 protein, a nucleic acid encoding the TASA peptide, a nucleic acid encoding DLK1 protein, or a composition including a plurality of immunogenic TASA peptides) that alone, or together with one or more additional agents, induces the desired response, such as, for example, induction of an immune response and/or treatment of a tumor in a subject. Ideally, a therapeutically effective amount provides a therapeutic effect without causing a substantial cytotoxic effect in the subject.

In one example, a desired response is to decrease the size, volume, or number (such as metastases) of a tumor in a subject. For example, the agent or agents can decrease the size, volume, or number of tumors by a desired amount, for example by at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 50%, at least 75%, at least 90%, or at least 95% as compared to a response in the absence of the agent.

Several preparations disclosed herein are administered in therapeutically effective amounts. A therapeutically effective amount of an immunogenic TASA peptide, a DLK1 protein, a nucleic acid encoding the TASA peptide, a nucleic acid encoding DLK1 protein, or composition including a plurality of immunogenic TASA peptides that is administered to a human or veterinary subject will vary depending upon a number of factors associated with that subject, for example the overall health of the subject. A therapeutically effective amount of the immunogenic TASA peptide, a DLK1 protein, a nucleic acid encoding the TASA peptide, a nucleic acid encoding DLK1 protein, or composition including a plurality of immunogenic polypeptides can be determined by varying the dosage and measuring the resulting therapeutic response, such as the regression of a tumor. Therapeutically effective amounts also can be determined through various *in vitro*, *in vivo* or *in situ* immunoassays. The disclosed agents can be administered in a single dose, or in several doses, as needed to obtain the desired response. However, the therapeutically effective amount can be dependent on the source applied, the subject being treated, the severity and type of the condition being treated, and the manner of administration.

Treating or Treatment: A therapeutic intervention (e.g., administration of a therapeutically effective amount of an immunogenic TASA peptide or composition including a plurality of immunogenic polypeptides) that ameliorates a sign or symptom of a disease or pathological condition related to a disease (such as a tumor). Treatment can also induce remission or cure of a condition, such as a tumor. In particular examples, treatment includes preventing a tumor, for example by inhibiting the full development of a tumor, such as preventing development of a metastasis or the development of a primary tumor. Prevention does not require a total absence of a tumor.

Reducing a sign or symptom associated with a tumor can be evidenced, for example, by a delayed onset of clinical symptoms of the disease in a susceptible subject (such as a subject having a tumor which has not yet metastasized), a

reduction in severity of some or all clinical symptoms of the disease, a slower progression of the disease (for example by prolonging the life of a subject having tumor), a reduction in the number of relapses of the disease, an improvement in the overall health or well-being of the subject, or by other parameters well known in the art that are specific to the particular tumor.

Vector: A nucleic acid molecule as introduced into a host cell, thereby producing a transformed host cell. A vector may include nucleic acid sequences that permit it to replicate in a host cell, such as an origin of replication. A vector may also include one or more selectable marker gene and other genetic elements known in the art. Vectors include plasmid vectors, including plasmids for expression in gram negative and gram positive bacterial cell. Exemplary vectors include those for expression in *E. coli*. Vectors also include viral vectors, such as, but are not limited to, retroviral, pox, adenoviral, herpes virus, alpha virus, baculovirus, Sindbis virus, vaccinia virus and poliovirus vectors.

Under conditions sufficient for: A phrase that is used to describe any environment that permits a desired activity. In one example the desired activity is formation of an immune complex. In particular examples the desired activity is treatment of a tumor.

Vascularization: The amount and type of blood vessels in a tissue or a cancer. Vascularization can be measured by a variety of methods, including histological methods. Tumor blood vessels have perivascular detachment, vessel dilation, and irregular shape. It is believed tumor blood vessels are not smooth like normal tissues, and are not ordered sufficiently to give oxygen to all of the tissues. If vascularization is "normalized" it is returned to a form in a normal (wildtype, not affected by disease), so that it is more ordered and reduced.

Unless otherwise explained, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure belongs. The singular terms "a," "an," and "the" include plural referents unless context clearly indicates otherwise. Similarly, the word "or" is intended to include "and" unless the context clearly indicates otherwise. It is further to be understood that all base sizes or amino acid sizes, and all molecular weight or molecular mass values, given for nucleic acids or polypeptides are approximate, and are provided for description. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of this disclosure, suitable methods and materials are described below. The term "comprises" means "includes." All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including explanations of terms, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Immunogenic TASA Peptides

Isolated polypeptides disclosed herein that include at most twelve amino acids from a tumor associated stromal cell antigen, such as Protein Delta Homolog 1 (DLK1; SEQ ID NO: 21), Hemoglobin Subunit Beta (HBB; SEQ ID NO: 22), Neuropilin 1 (NRP1; SEQ ID NO: 23), Tumor Endothelial Marker 1 (TEM1; SEQ ID NO: 24), Ephrin Type A Receptor 2 (EphA2; SEQ ID NO: 25), Regulator of G-Protein Signaling 5 (RGS5; SEQ ID NO: 26), Platelet Derived Growth Factor Receptor β (PDGFR β ; SEQ ID NO: 27), melanoma chondroitin sulfate proteoglycan (NG2; SEQ ID NO: 28), Neuropilin 2 (NRP2; SEQ ID NO: 29), Glutamate Carbox-

ypeptidase 2, (PSMA; SEQ ID NO: 30), Vascular Endothelial Growth Factor 1 (VEGFR1; SEQ ID NO: 31), Vascular Endothelial Growth Factor Receptor 2 (VEGFR2; SEQ ID NO: 32). These polypeptides include an antigenic determinant from a TASA and are immunogenic, and thus can be used to induce an immune response in a subject.

The isolated TASA peptides, can be chemically synthesized by standard methods. If desired, polypeptides can also be chemically synthesized by emerging technologies. One such process is described in W. Lu et al., *Federation of European Biochemical Societies Letters*. 429:31-35, 1998. Polypeptides can also be produced using molecular genetic techniques, such as by inserting a nucleic acid encoding a TASA peptide or an epitope thereof into an expression vector, introducing the expression vector into a host cell, and isolating the polypeptide (see below).

The immunogenic TASA peptides include at most twelve amino acids, such as nine, ten, eleven or twelve consecutive amino acids of a TASA. For example, in some embodiments, the immunogenic TASA peptides includes at most twelve

amino acids, at most eleven amino acids, at most ten amino acids or at most nine amino acids, wherein the polypeptide includes an amino acid sequence as shown in Table 1. In other embodiments, an immunogenic TASA peptide comprises or consists of DLK1₁₅₈₋₁₆₆ (CPPGFSGNF, SEQ ID NO: 65), DLK1₁₆₁₋₁₆₉ (GFSGNFCEI, SEQ ID NO: 66), or at least 9, 10, 11 or 12 amino acids of DLK1₂₅₉₋₂₇₀ and/or DLK1₂₆₂₋₂₇₀ (TILGVLTSLVV, SEQ ID NO: 67 includes both of these epitopes). These immunogenic DLK1 peptides can be used individually. However, a combination of two or more of these DLK1 peptides can be utilized. In additional embodiments, the immunogenic TASA peptides includes at most twelve amino acids, at most eleven amino acids, at most ten amino acids or at most nine amino acids of an amino acid sequence as shown in Table 1. These TASA peptides can be used individually or in combination.

In several embodiments, the amino acid at position 2 of the immunogenic TASA peptide is substituted for a valine residue. In additional embodiments, the amino acid at position 9 of the immunogenic TASA peptide is substituted for a leucine residue.

TABLE 1

Immunogenic TASA Peptides.				
TASA Protein	Accession No.*	TASA Peptide	AA Positions	SEQ ID NO.
DLK1	NP_003827.3	RLTPGVHEX ₁ wherein X ₁ is a leucine or a valine	269-277	1
		ILGVLTSLV	310-318	2
		FLNKCEWV	326-334	3
HBB	CAG46711.1	RLLVVYPWVX ₂ wherein X ₂ is a threonine or a valine	31-39	4
		RLLGNVLVX ₃ V wherein X ₃ is a cysteine or a valine	105-114	5
NRP1	CAI16997.1	GLLRFTAV	331-339	6
		GX ₄ LGMVSGV wherein X ₄ is a leucine or a methionine	433-441	7
		VLLGAVCGV	869-877	8
TEM1	AAG00867.1	LLVPTCVFX ₅ V wherein X ₅ is a leucine or a valine	691-700	9
EphA2	NP_004422.2	TLADFDPRV	883-891	10
RGS5	AAB84001.1	LX ₆ ALPHSCL wherein X ₆ is a leucine or an alanine	5-13	11
PDGFRβ	AAA60049.1	ILLWEIFTX ₇ wherein X ₇ is L or V	890-898	12
NG2	AAQ62842	X ₈ LSNLSFPV wherein X ₈ is I or T	770-778	13
		LILPLLFYL	2238-2246	14
NRP2	NP_957718.1	DIWDGIPHV	214-222	15
		YLQVDLRFL	328-336	16
		NMLGMLSGV	436-444	17
PSMA	NP_004467.1	LLQERGVAYI	441-450	18
VEGFR1	NP_002010.2	TLFWLLLT	770-778	19
VEGFR2	NP_002244.1	VIAMFFWLL	773-781	20

*Accession No. NP_003827.3 incorporated by reference herein as of Sep. 11, 2011; Accession No. CAG46711.1 incorporated by reference herein as of Oct. 16, 2008; Accession No. CAI16997.1 incorporated by reference herein as of Jan. 13, 2009; Accession No. AAG00867.1 incorporated by reference herein as of Aug. 23, 2000; Accession No. NP_004422.2 incorporated by reference herein as of Aug. 13, 2011; Accession No. AAB84001.1 incorporated by reference herein as of Nov. 8, 1997; Accession No. AAA60049.1 incorporated by reference herein as of Jan. 7, 1995; Accession No. NP_957718.1 incorporated by reference herein as of Aug. 21, 2011; Accession No. NP_004467.1 incorporated by reference herein as of Sep. 24, 2011; Accession No. NP_002010.2 incorporated by reference herein as of Sep. 25, 2011; Accession No. NP_002244.1 incorporated by reference herein as of Sep. 25, 2011.

Without being bound by theory, it is believed that the presentation of peptides by MHC Class I molecules involves binding to the cleft in an MHC Class I molecule through the anchor residues of the peptide and ultimate presentation on the cell surface. Depending upon the particular anchor residues, among other things, certain peptides can bind more tightly to particular HLA molecules than others. Peptides that bind well are usually "dominant" epitopes, while those that bind less well are often "subdominant" or "cryptic" epitopes. Dominant epitopes of either self proteins or foreign proteins evoke strong tolerance or immune responses. Subdominant or cryptic epitopes generate weak responses or no responses at all. Without being bound by theory, tighter binding by dominant epitopes to HLA molecules results in their denser presentation on the cell surface, greater opportunity to react with immune cells and greater likelihood of eliciting an immune response or tolerance. MHC Class I molecules present epitopes from endogenous proteins for presentation to CTL cells. HLA A, HLA B and HLA C molecules bind peptides of about eight to ten amino acids in length (such as nine amino acids in length) that have particular anchoring residues. The anchoring residues recognized by an HLA Class I molecule depend upon the particular allelic form of the HLA molecule. A CD8+ T cell bears T cell receptors that recognize a specific epitope when presented by a particular HLA molecule on a cell. When a CTL precursor that has been stimulated by an antigen presenting cell to become a cytotoxic T lymphocyte contacts a cell that bears such an HLA-peptide complex, the CTL forms a conjugate with the cell and destroys it. In several examples presented herein, the immunogenic TASA peptides that are disclosed bind and are presented by HLA-A2.

Thus, in some examples, an isolated polypeptide includes at most 9, 10, 11 or 12 amino acids from DLK1, wherein the polypeptide includes an amino acid sequence set forth as RLTPGVHEX₁ (SEQ ID NO: 1) wherein X₁ is a leucine (L) or a valine (V). In some embodiments amino acid X₁ is a leucine (L). In other embodiments, amino acid X₁ is a valine (V). In one example the polypeptide consists of the amino acid sequence set forth as SEQ ID NO: 1. Thus, in one example, the polypeptide consists of SEQ ID NO: 1, wherein amino acid X₁ is a valine (V). In another example the polypeptide consists of SEQ ID NO: 1, wherein amino acid X₁ is a leucine (L).

In other examples, an isolated polypeptide includes at most 9, 10, 11 or 12 amino acids from DLK1, wherein the polypeptide includes an amino acid sequence set forth as ILGVLTSLV (SEQ ID NO: 2). In one example the polypeptide consists of the amino acid sequence set forth as SEQ ID NO: 2.

In additional examples, an isolated polypeptide includes at most 9, 10, 11 or 12 amino acids from DLK1, wherein the polypeptide includes an amino acid sequence set forth as FLNKCETWV (SEQ ID NO: 3). In one example the polypeptide consists of the amino acid sequence set forth as SEQ ID NO: 3.

In yet other examples, an isolated polypeptide that includes an isolated polypeptide includes at most 9, 10, 11 or 12 amino acids from DLK1, wherein the polypeptide includes one of SEQ ID NO: 65, SEQ ID NO: 66, or SEQ ID NO: 67. In several examples, the polypeptide consists of the amino acid sequence set forth as one of SEQ ID NO: 65, SEQ ID NO: 66 or SEQ ID NO: 67.

In further examples, an isolated polypeptide includes at most 9, 10, 11 or 12 amino acids from HBB, wherein the polypeptide includes an amino acid sequence set forth as RLLVYPWX₂ (SEQ ID NO: 4) wherein X₂ is a threonine (T) or a valine (V). In further embodiments amino acid X₂ is

a threonine (T). In other embodiments, amino acid X₂ is a valine (V). In one example the polypeptide consists of the amino acid sequence set forth as SEQ ID NO: 4. Thus, in one example, the polypeptide consists of SEQ ID NO: 4, wherein amino acid X₂ is a valine (V), and in another example the polypeptide consists of SEQ ID NO: 4, wherein amino acid X₂ is a threonine (T).

In still other examples, an isolated polypeptide includes at most 9, 10, 11 or 12 amino acids from HBB, wherein the polypeptide includes an amino acid sequence set forth as RLLGNVLVX₃V (SEQ ID NO: 5) wherein X₃ is a cysteine (C) or a valine (V). In additional embodiments amino acid X₃ is a cysteine (C). In other embodiments, amino acid X₃ is a valine (V). In one example the polypeptide consists of the amino acid sequence set forth as SEQ ID NO: 5. Thus, in one example, the polypeptide consists of SEQ ID NO: 5, wherein amino acid X₃ is a valine (V), and in another example the polypeptide consists of SEQ ID NO: 5, wherein amino acid X₃ is a cysteine (C).

In some examples, an isolated polypeptide includes at most 9, 10, 11 or 12 amino acids from NRP1, wherein the polypeptide includes an amino acid sequence set forth as GLLRFVTAV (SEQ ID NO: 6). In one example the polypeptide consists of the amino acid sequence set forth as SEQ ID NO: 6.

In additional examples, an isolated polypeptide includes at 9, 10, 11 or 12 twelve amino acids from NRP1, wherein the polypeptide includes an amino acid sequence set forth as GX₄LGMVSG (SEQ ID NO: 7) wherein X₄ is a leucine (L) or a methionine (M). In still other embodiments, amino acid X₄ is a leucine (L). In other embodiments, amino acid X₄ is a methionine (M). In one example the polypeptide consists of the amino acid sequence set forth as SEQ ID NO: 7. Thus, in one example, the polypeptide consists of SEQ ID NO: 7, wherein amino acid X₄ is a methionine (M), and in another example the polypeptide consists of SEQ ID NO: 7, wherein amino acid X₄ is a leucine (L).

In further examples, an isolated polypeptide includes at most 9, 10, 11 or 12 amino acids from NRP1, wherein the polypeptide includes an amino acid sequence set forth as VLLGAVCGV (SEQ ID NO: 8). In one example the polypeptide consists essentially of the amino acid sequence set forth as SEQ ID NO: 8. In additional examples, the polypeptide is eleven amino acids in length, ten amino acids in length or nine amino acids in length. In further examples, the isolated polypeptide consists of the amino acid sequence set forth as SEQ ID NO: 8.

In other examples, an isolated polypeptide includes at most 9, 10, 11 or 12 amino acids from TEM1, wherein the polypeptide includes an amino acid sequence set forth as LLVPTCVFX₅V (SEQ ID NO: 9) wherein X₅ is a leucine (L) or a valine (V). In some embodiments, amino acid X₅ is a leucine (L). In other embodiments, amino acid X₅ is a valine (V). In one example the polypeptide consists of the amino acid sequence set forth as SEQ ID NO: 9. Thus, in one example, the polypeptide consists of SEQ ID NO: 9, wherein amino acid X₅ is a valine (V), and in another example the polypeptide consists of SEQ ID NO: 9, wherein amino acid X₅ is a leucine (L).

In additional examples, an isolated polypeptide includes at most 9, 10, 11 or 12 amino acids from EphA2, wherein the polypeptide includes an amino acid sequence set forth as TLADFDP (SEQ ID NO: 10). In one example the polypeptide consists of the amino acid sequence set forth as SEQ ID NO: 10.

In some examples, an isolated polypeptide includes at most 9, 10, 11 or 12 amino acids from RGS5, wherein the polypep-

tide includes an amino acid sequence set forth as LX₆ALPHSCL (SEQ ID NO: 11) wherein X₆ is a leucine (L) or an alanine (A). In further embodiments, amino acid X₆ is a leucine (L). In other embodiments, amino acid X₆ is an alanine (A). In one example the polypeptide consists of the amino acid sequence set forth as SEQ ID NO: 11. Thus, in one example, the polypeptide consists of SEQ ID NO: 11, wherein amino acid X₆ is an alanine (A), and in another example the polypeptide consists of SEQ ID NO: 11, wherein amino acid X₆ is a leucine (L).

In other examples, an isolated polypeptide includes at most 9, 10, 11 or 12 amino acids from PDGFR β , wherein the polypeptide includes an amino acid sequence set forth as ILLWEIFTX₇ (SEQ ID NO: 12) wherein X₇ is a leucine (L) or a valine (V). In some embodiments, amino acid X₇ is a leucine (L). In other embodiments, amino acid X₇ is a valine (V). In one example the polypeptide consists of the amino acid sequence set forth as SEQ ID NO: 12. Thus, in one example, the polypeptide consists of SEQ ID NO: 12, wherein amino acid X₇ is a valine (V), and in another example the polypeptide consists of SEQ ID NO: 12, wherein amino acid X₇ is a leucine (L).

TABLE A

The following lists certain TASA peptides:		
TASA Protein	TASA Peptide	SEQ ID NO
DLK1	RLTPGVHEL	68
	RLTPGVHEV	69
	ILGVLTSLV	2
	FLNKCETWV	3
HBB	RLLVVYPWT	70
	RLLVVYPWV	71
	RLLGNVLVCV	72
	RLLGNVLVVV	73
NRP1	GLLRFVTAV	6
	GLLGMVSGL	74
	GMLGMVSGL	75
	VLLGAVCGV	8
TEM1	LLVPTCVFLV	76
	LLVPTCVFVV	77
EphA2	TLADFDPRV	10
RGS5	LLALPHSCL	78
	LAALPHSCL	79
PDGFR β	ILLWEIFTV	80
	ILLWEIFTL	81
NG2	ILSNLSFPV	82
	TLNLSFPV	83
	LILPLLFYL	14
NRP2	DIWDGIPHV	15
	YLQVDLRFL	16
	NMLGMLSGL	17
PSMA	LLQERGVAI	18
VEGFR1	TLFWLLLTLL	19
VEGFR2	VIAMFFWLL	20

In several embodiments, an immunogenic TASA peptide is included in a fusion protein. For example, each of the immunogenic TASA peptides included in a composition including a plurality of immunogenic TASA peptides (described herein) can be in the form of a fusion protein. Thus, the fusion

protein can include an immunogenic TASA peptide and a second heterologous moiety, such as a myc protein, an enzyme or a carrier (such as a hepatitis carrier protein or bovine serum albumin) covalently linked to the immunogenic TASA peptide. A second heterologous moiety can be covalently or non-covalently linked to the immunogenic TASA peptide.

In additional embodiments, the immunogenic TASA peptides can be included in a fusion protein and can also include heterologous sequences. Thus, in several specific non-limiting examples, one or more of the immunogenic TASA peptides are included in a fusion polypeptide, for example a fusion of an immunogenic TASA peptide with six sequential histidine residues, a β -galactosidase amino acid sequence, or an immunoglobulin amino acid sequence. The immunogenic TASA peptides can also be covalently linked to a carrier. Suitable carriers include, but are not limited to, a hepatitis B small envelope protein HBsAg. This protein has the capacity to self assemble into aggregates and can form viral-like particles. The preparation of HBsAg is well documented, see for example European Patent Application Publication No. EP-A-0 226 846, European Patent Application Publication No. EP-A-0 299 108 and PCT Publication No. WO 01/117554, and the amino acid sequence disclosed, for example, in Tiollais et al., Nature, 317: 489, 1985, and European Patent Publication No. EP-A-0 278 940, and PCT Publication No. WO 91/14703, all of which are incorporated herein by reference.

The fusion polypeptide can optionally include repetitions of one or more of any of the immunogenic TASA peptides disclosed herein. In one specific, non-limiting example, the fusion polypeptide includes two, three, four, five, or up to ten repetitions of an immunogenic TASA peptide. In another example, the fusion polypeptide can optionally include two or more different immunogenic TASA peptides disclosed herein, for example an immunogenic DLK1 peptide and an immunogenic TEM1 peptide. In one specific, non-limiting example, the fusion polypeptide includes two, three, four, five, or up to ten different immunogenic TASA peptides. A linker sequence can optionally be included between the immunogenic TASA peptides. In all of these examples, the polypeptide does not include the full-length TASA amino acid sequence.

In some embodiments, two or more different immunogenic TASA peptides can be included on a polypeptide, such as an immunogenic molecule. For example, 2-20 or more different immunogenic TASA peptides can be included in the polypeptide, such as 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more different immunogenic TASA peptides. The different immunogenic TASA peptides can be separated by peptide linkers. In some examples, several copies of the same immunogenic TASA peptide can be included in a polypeptide, such as an immunogenic molecule. For example a repeat of a immunogenic TASA peptide in series. In some examples, two, three, four, five or more copies of the same immunogenic TASA peptide are included in an polypeptide. In examples wherein two or more immunogenic TASA peptide are included on a polypeptide, the immunogenic TASA peptides can be separated by peptide linkers.

In additional embodiments, a plurality of the immunogenic TASA peptides described above is included in a composition. In one embodiment, the composition includes a plurality of immunogenic TASA peptides, wherein each immunogenic TASA peptide in the plurality is at most twelve amino acids in length, wherein the plurality of peptides includes at least two different immunogenic TASA peptides. Thus the composition can include 2, 3, 4, 5, 6, 7, 8, 9, 10 or more of the immunogenic TASA peptides disclosed in Table 1. In some

embodiments, the composition includes 2, 3, 4, 5, 6 or 7 immunogenic peptides each from a different TASA. In other embodiments, the composition includes 2, 3, 4, 5, 6, 7, 8, 9 or 10 immunogenic peptides from 2, 3, 4, 5 or 6 different TASAs.

Compositions including a plurality of immunogenic TASA peptides described herein can include varying concentrations of different concentrations of each immunogenic TASA peptide in the plurality of immunogenic TASA peptides. For example, in some embodiments, the composition includes two, three, four, five, six, or seven different types of immunogenic TASA peptide in an equimolar ratio. In other examples, the composition includes two, three, four, five, six, or seven different types of immunogenic TASA peptide in a non-equimolar ratio.

In some embodiments, the composition includes immunogenic peptides from DLK1, HBB, NRP1 and TEM1. In other embodiments, the composition includes immunogenic peptides from DLK1, HBB, NRP1, TEM1, EphA2 and RGS5. In still other embodiments, the composition includes immunogenic peptides from DLK1, HBB, NRP1, TEM1, EphA2, RGS5 and PDGFR β .

In some embodiments, a composition is provided including a plurality of immunogenic TASA peptides, wherein each immunogenic TASA peptide in the plurality is at most twelve amino acids in length, wherein the plurality of immunogenic TASA peptides includes at least one polypeptide including an amino acid sequence as shown for one of the DLK1 peptides listed in Table 1, at least one polypeptide including an amino acid sequence as shown for one of the HBB peptides listed in Table 1, at least one polypeptide including an amino acid sequence as shown for one of the NRP1 peptides listed in Table 1, and at least one polypeptide including an amino acid sequence as shown for one of the TEM1 peptides listed in Table 1. In some such embodiments, the plurality of polypeptides further includes at least one polypeptide including an amino acid sequence as shown for the EphA2 peptide listed in Table 1, and at least one polypeptide including an amino acid sequence as shown for one of the RGS5 peptides listed in Table 1. In still more embodiments, the plurality of polypeptides further includes at least one polypeptide including an amino acid sequence as shown for the EphA2 peptide listed in Table 1, at least one polypeptide including an amino acid sequence as shown for one of the RGS5 peptides listed in Table 1, and at least one polypeptide including an amino acid sequence as shown for one of the PDGFR β peptides listed in Table 1. In some such embodiments, each polypeptide in the plurality of polypeptides is nine, ten, eleven or twelve amino acids in length.

In some embodiments, a composition is provided including a plurality of immunogenic TASA peptides including a polypeptide consisting of an amino acid sequence as shown for one of the DLK1 peptides listed in Table 1, a polypeptide consisting of an amino acid sequence as shown for one of the HBB peptides listed in Table 1, a polypeptide consisting of an amino acid sequence as shown for one of the NRP1 peptides listed in Table 1, and a polypeptide consisting of an amino acid sequence as shown for one of the TEM1 peptides listed in Table 1. In some embodiments, the composition further includes a polypeptide consisting of an amino acid sequence as shown for the EphA2 peptide listed in Table 1, and a polypeptide consisting of an amino acid sequence as shown for one of the RGS5 peptides listed in Table 1. In still more embodiments, the composition further includes a polypeptide consisting of an amino acid sequence as shown for the EphA2 peptide listed in Table 1, a polypeptide consisting of an amino acid sequence as shown for one of the RGS5 peptides listed in

Table 1, and a polypeptide consisting of an amino acid sequence as shown for one of the PDGFR β polypeptides listed in Table 1. In some such embodiments, each polypeptide in the plurality of polypeptides is nine, ten, eleven or twelve amino acids in length.

In some embodiments, a composition is provided including a plurality of immunogenic TASA peptides including a peptide comprising an amino acid sequence set forth as SEQ ID NO: 1, a peptide comprising an amino acid sequence set forth as SEQ ID NO: 2 and a peptide comprising an amino acid sequence set forth as SEQ ID NO: 3. In other embodiments, a composition is provided including a plurality of immunogenic TASA peptides including a peptide comprising an amino acid sequence set forth as SEQ ID NO: 4 and a peptide comprising an amino acid sequence set forth as SEQ ID NO: 5. In still other embodiments, a composition is provided including a plurality of immunogenic TASA peptides including a peptide comprising an amino acid sequence set forth as SEQ ID NO: 6, a peptide comprising an amino acid sequence set forth as SEQ ID NO: 7 and a peptide comprising an amino acid sequence set forth as SEQ ID NO: 8. In some such embodiments, each polypeptide in the plurality of polypeptides is nine, ten, eleven or twelve amino acids in length.

In some embodiments, a composition is provided including a plurality of immunogenic TASA peptides including a DLK1 polypeptide comprising an amino acid sequence set forth as FLNKCETWV (SEQ ID NO: 3), a HBB polypeptide comprising an amino acid sequence set forth as RLLV-VYPWX₂ (SEQ ID NO: 4) wherein X₂ is a threonine (T), a NRP1 polypeptide comprising an amino acid sequence set forth as VLLGAVCGV (SEQ ID NO: 8), a TEM1 polypeptide comprising an amino acid sequence set forth as LLVPTCVFX₅V (SEQ ID NO: 9) wherein X₅ is a leucine (L), an EphA2 polypeptide comprising an amino acid sequence set forth as TLADFDPRV (SEQ ID NO: 10), a RGS5 polypeptide comprising an amino acid sequence set forth as LX₆ALPHSCL (SEQ ID NO: 11) wherein X₆ is an alanine (A), a PDGFR β polypeptide comprising an amino acid sequence set forth as ILLWEIFTX₇ (SEQ ID NO: 12) wherein X₇ is a leucine (L). In some such embodiments, each polypeptide in the plurality of polypeptides is at least nine, at least ten, at least eleven or at least twelve amino acids in length.

In some embodiments, a composition is provided including a plurality of immunogenic TASA peptides, wherein the plurality of immunogenic TASA peptides includes a DLK1 polypeptide consisting of an amino acid sequence set forth as FLNKCETWV (SEQ ID NO: 3), a HBB polypeptide consisting of an amino acid sequence set forth as RLLV-VYPWX₂ (SEQ ID NO: 4) wherein X₂ is a threonine (T), a NRP1 polypeptide consisting of an amino acid sequence set forth as VLLGAVCGV (SEQ ID NO: 8) and a TEM1 polypeptide consisting of an amino acid sequence set forth as LLVPTCVFX₅V (SEQ ID NO: 9) wherein X₅ is a leucine (L). In some embodiments, the composition further includes an EphA2 polypeptide consisting of an amino acid sequence set forth as TLADFDPRV (SEQ ID NO: 10) and a RGS5 polypeptide consisting of an amino acid sequence set forth as LX₆ALPHSCL (SEQ ID NO: 11) wherein X₆ is an alanine (A). In some embodiments, the composition further includes an EphA2 polypeptide consisting of an amino acid sequence set forth as TLADFDPRV (SEQ ID NO: 10), a RGS5 polypeptide consisting of an amino acid sequence set forth as LX₆ALPHSCL (SEQ ID NO: 11) wherein X₆ is an alanine (A) and a PDGFR β polypeptide consisting of an amino acid sequence set forth as ILLWEIFTX₇ (SEQ ID NO: 12)

wherein X₇ is a leucine (L). In some such embodiments, each polypeptide in the plurality of polypeptides is at least nine, at least ten, at least eleven or at least twelve amino acids in length.

The immunogenic TASA peptides can be covalently linked to a carrier, which is an immunogenic macromolecule to which an antigenic molecule can be bound. When bound to a carrier, the bound polypeptide becomes more immunogenic. Carriers are chosen to increase the immunogenicity of the bound molecule and/or to elicit higher titers of antibodies against the carrier which are diagnostically, analytically, and/or therapeutically beneficial. Covalent linking of a molecule to a carrier can confer enhanced immunogenicity and T cell dependence (see Pozsgay et al., *PNAS* 96:5194-97, 1999; Lee et al., *J. Immunol.* 116:1711-18, 1976; Dintzis et al., *PNAS* 73:3671-75, 1976). Useful carriers include polymeric carriers, which can be natural (for example, polysaccharides, polypeptides or proteins from bacteria or viruses), semi-synthetic or synthetic materials containing one or more functional groups to which a reactant moiety can be attached. Bacterial products and viral proteins (such as hepatitis B surface antigen and core antigen) can also be used as carriers, as well as proteins from higher organisms such as keyhole limpet hemocyanin, horseshoe crab hemocyanin, edestin, mammalian serum albumins, and mammalian immunoglobulins. Additional bacterial products for use as carriers include bacterial wall proteins and other products (for example, streptococcal or staphylococcal cell walls and lipopolysaccharide (LPS)).

Protein Delta Homolog 1 (DLK1)

In some embodiments, the methods disclosed herein utilize DLK1 protein, or a nucleic acid encoding DLK1 protein. An exemplary DLK1 protein is set forth as SEQ ID NO: 21, see also GENBANK® Accession No. NP_003827.3, incorporated herein by reference, and GENBANK® Accession No. NM_003836.5 (Sep. 23, 2012), incorporated herein by reference. In some embodiments, the DLK1 protein is at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99% identical to SEQ ID NO: 21. Human DLK1 has very high homology with DLK1 from other animal species and therefore, the sequences of DLK1 from other organisms can be utilized, particularly where these sequences are identical, substantially homologous, and elicit an effective immune response against the target antigen (e.g., native DLK1 expressed by a cell). Additional exemplary DLK1 proteins include at most 10, at most 9, at most 8, at most 7, at most 6, at most 5, at most 4, at most 3, at most 2 or at most 1 conservative amino acid substitutions in SEQ ID NO: 21. The methods disclosed herein can utilize protein fragments of DLK1 protein, such as 100, 150, 200, 250, 300, 350 or 380 amino acids of a DLK1 protein.

In several embodiments, the isolated DLK1 protein or polypeptide is included in a fusion protein. Thus, the fusion protein can include the DLK1 protein or DLK1 polypeptide (see above) and a second heterologous moiety, such as a myc protein, an enzyme or a carrier (such as a hepatitis carrier protein or bovine serum albumin) covalently linked to the DLK1 protein or polypeptide. Thus, in several specific non-limiting examples, the fusion protein includes a DLK1 protein and six sequential histidine residues, a β -galactosidase amino acid sequence, and/or an immunoglobulin amino acid sequence. However, in other embodiments, the DLK1 is not fused to a heterologous moiety.

DLK1 proteins or polypeptides that are linked to a carrier are also of use in the disclosed methods. Generally, a carrier is an immunogenic macromolecule to which an antigenic molecule can be bound. When bound to a carrier, the bound DLK1 protein or DLK1 polypeptide becomes more immunogenic. Carriers are chosen to increase the immunogenicity of the bound molecule and/or to elicit higher titers of antibodies against the carrier which are diagnostically, analytically, and/or therapeutically beneficial. Covalent linking of a molecule to a carrier can confer enhanced immunogenicity and T cell dependence (see Pozsgay et al., *PNAS* 96:5194-97, 1999; Lee et al., *J. Immunol.* 116:1711-18, 1976; Dintzis et al., *PNAS* 73:3671-75, 1976). Useful carriers include polymeric carriers, which can be natural (for example, polysaccharides, polypeptides or proteins from bacteria or viruses), semi-synthetic or synthetic materials containing one or more functional groups to which a reactant moiety can be attached. Bacterial products and viral proteins (such as hepatitis B surface antigen and core antigen) can also be used as carriers, as well as proteins from higher organisms such as keyhole limpet hemocyanin, horseshoe crab hemocyanin, edestin, mammalian serum albumins, and mammalian immunoglobulins. Suitable carriers include, but are not limited to, a hepatitis B small envelope protein HBsAg. This protein has the capacity to self-assemble into aggregates and can form viral-like particles. The preparation of HBsAg is well documented, see for example European Patent Application Publication No. EP-A-0 226 846, European Patent Application Publication No. EP-A-0 299 108 and PCT Publication No. WO 01/117554, and the amino acid sequence disclosed, for example, in Tiollais et al., *Nature*, 317: 489, 1985, and European Patent Publication No. EP-A-0 278 940, and PCT Publication No. WO 91/14703, all of which are incorporated herein by reference.

In other embodiments, only the DLK1 protein or polypeptide is utilized. Thus, a second heterologous moiety is non-covalently linked to the DLK1 protein or polypeptide.

Nucleotides, Expression Vectors and Host Cells

Nucleic acids encoding one or more of the immunogenic TASA peptides, or encoding DLK1 protein, are provided. These polynucleotides include DNA, cDNA and RNA sequences which encode the polypeptide(s) of interest. Nucleic acid molecules encoding these peptides can readily be produced by one of skill in the art, using the amino acid sequences provided herein, and the genetic code. In addition, one of skill can readily construct a variety of clones containing functionally equivalent nucleic acids, such as nucleic acids which differ in sequence but which encode the same effector molecule, detectable marker or antibody sequence. An exemplary nucleic acid sequence encoding a DLK1 protein is provided in GENBANK® Accession No. NM_003836.5 (Sep. 23, 2012), incorporated herein by reference).

Nucleic acid sequences encoding one or more of the immunogenic TASA peptides can be prepared by any suitable method including, for example, cloning of appropriate sequences or by direct chemical synthesis by methods such as the phosphotriester method of Narang et al., *Meth. Enzymol.* 68:90-99, 1979; the phosphodiester method of Brown et al., *Meth. Enzymol.* 68:109-151, 1979; the diethylphosphoramidite method of Beaucage et al., *Tetra. Lett.* 22:1859-1862, 1981; the solid phase phosphoramidite triester method described by Beaucage & Caruthers, *Tetra. Letts.* 22(20): 1859-1862, 1981, for example, using an automated synthesizer as described in, for example, Needham-VanDevanter et

al., *Nucl. Acids Res.* 12:6159-6168, 1984; and, the solid support method of U.S. Pat. No. 4,458,066. Chemical synthesis produces a single stranded oligonucleotide. This can be converted into double stranded DNA by hybridization with a complementary sequence, or by polymerization with a DNA polymerase using the single strand as a template.

Exemplary nucleic acids including sequences encoding one or more of the immunogenic TASA peptides can be prepared by cloning techniques. Examples of appropriate cloning and sequencing techniques, and instructions sufficient to direct persons of skill through cloning are found in Sambrook et al., supra, Berger and Kimmel (eds.), supra, and Ausubel, supra. Product information from manufacturers of biological reagents and experimental equipment also provide useful information. Such manufacturers include the SIGMA Chemical Company (Saint Louis, Mo.), R&D Systems (Minneapolis, Minn.), Pharmacia Amersham (Piscataway, N.J.), CLONTECH Laboratories, Inc. (Palo Alto, Calif.), Chem Genes Corp., Aldrich Chemical Company (Milwaukee, Wis.), Glen Research, Inc., GIBCO BRL Life Technologies, Inc. (Gaithersburg, Md.), Fluka Chemica-Biochemika Analytika (Fluka Chemie AG, Buchs, Switzerland), Invitrogen (San Diego, Calif.), and Applied Biosystems (Foster City, Calif.), as well as many other commercial sources known to one of skill.

Nucleic acids can also be prepared by amplification methods. Amplification methods include polymerase chain reaction (PCR), the ligase chain reaction (LCR), the transcription-based amplification system (TAS), the self-sustained sequence replication system (3SR). A wide variety of cloning methods, host cells, and in vitro amplification methodologies are well known to persons of skill.

Once the nucleic acids encoding one or more of the immunogenic TASA peptides are isolated and cloned, the protein can be expressed in a recombinantly engineered cell such as bacteria, plant, yeast, insect and mammalian cells using a suitable expression vector. One or more DNA sequences encoding one or more immunogenic TASA peptide can be expressed in vitro by DNA transfer into a suitable host cell. The cell may be prokaryotic or eukaryotic. The term also includes any progeny of the subject host cell. It is understood that all progeny may not be identical to the parental cell since there may be mutations that occur during replication. Methods of stable transfer, meaning that the foreign DNA is continuously maintained in the host, are known in the art.

Polynucleotide sequences encoding one or more of the immunogenic TASA peptides, can be operatively linked to expression control sequences (e.g., a promoter). An expression control sequence operatively linked to a coding sequence is ligated such that expression of the coding sequence is achieved under conditions compatible with the expression control sequences. The expression control sequences include, but are not limited to appropriate promoters, enhancers, transcription terminators, a start codon (i.e., ATG) in front of a protein-encoding gene, splicing signal for introns, maintenance of the correct reading frame of that gene to permit proper translation of mRNA, and stop codons.

The polynucleotide sequences encoding one or more of the immunogenic TASA peptides can be inserted into an expression vector including, but not limited to a plasmid, virus or other vehicle that can be manipulated to allow insertion or incorporation of sequences and can be expressed in either prokaryotes or eukaryotes. Hosts can include microbial, yeast, insect and mammalian organisms. Methods of expressing DNA sequences having eukaryotic or viral sequences in prokaryotes are well known in the art. Biologically functional

viral and plasmid DNA vectors capable of expression and replication in a host are known in the art.

Transformation of a host cell with recombinant DNA may be carried out by conventional techniques as are well known to those skilled in the art. Where the host is prokaryotic, such as *E. coli*, competent cells which are capable of DNA uptake can be prepared from cells harvested after exponential growth phase and subsequently treated by the CaCl_2 method using procedures well known in the art. Alternatively, MgCl_2 or RbCl can be used. Transformation can also be performed after forming a protoplast of the host cell if desired, or by electroporation.

When the host is a eukaryote, such methods of transfection of DNA as calcium phosphate coprecipitates, conventional mechanical procedures such as microinjection, electroporation, insertion of a plasmid encased in liposomes, or virus vectors may be used. Eukaryotic cells can also be cotransformed with polynucleotide sequences encoding one or more of the immunogenic TASA peptides, and a second foreign DNA molecule encoding a selectable phenotype, such as the herpes simplex thymidine kinase gene. Another method is to use a eukaryotic viral vector, such as simian virus 40 (SV40) or bovine papilloma virus, to transiently infect or transform eukaryotic cells and express the one or more of the immunogenic TASA peptides (see for example, *Eukaryotic Viral Vectors*, Cold Spring Harbor Laboratory, Gluzman ed., 1982). One of skill in the art can readily use expression systems such as plasmids and vectors of use in producing proteins in cells including higher eukaryotic cells such as the COS, CHO, HeLa and myeloma cell lines.

In some embodiments, one or more polynucleotides encoding one or more immunogenic TASA peptides are included in one or more viral vectors. Examples of suitable viral vectors include retrovirus vectors, pox vectors, adenoviral vectors, herpes virus vectors, alpha virus vectors, baculovirus vectors, Sindbis virus vectors, vaccinia virus vectors and poliovirus vectors. Basic techniques for preparing recombinant DNA viruses containing a heterologous DNA sequence are known in the art. Such techniques involve, for example, homologous recombination between the viral DNA sequences flanking the DNA sequence in a donor plasmid and homologous sequences present in the parental virus (Mackett et al., 1982, *Proc. Natl. Acad. Sci. USA* 79:7415-7419).

Viral vectors can be prepared encoding one or more of the immunogenic TASA peptides. A number of viral vectors have been constructed, including polyoma, SV40 (Madzak et al., *J. Gen. Virol.*, 73:1533-1536, 1992), adenovirus (Berkner, *Curr. Top. Microbiol. Immunol.*, 158:39-6, 1992; Berliner et al., *Bio Techniques*, 6:616-629, 1988; Gorziglia et al., *J. Virol.*, 66:4407-4412, 1992; Quantin et al., *Proc. Natl. Acad. Sci. USA*, 89:2581-2584, 1992; Rosenfeld et al., *Cell*, 68:143-155, 1992; Wilkinson et al., *Nucl. Acids Res.*, 20:2233-2239, 1992; Stratford-Perricaudet et al., *Hum. Gene Ther.*, 1:241-256, 1990), vaccinia virus (Mackett et al., *Biotechnology*, 24:495-499, 1991), adeno-associated virus (Muzyczka, *Curr. Top. Microbiol. Immunol.*, 158:91-123, 1992; On et al., *Gene*, 89:279-282, 1990), herpes viruses including HSV and EBV (Margolske, *Curr. Top. Microbiol. Immunol.*, 158:67-90, 1992; Johnson et al., *J. Virol.*, 66:2952-2965, 1992; Fink et al., *Hum. Gene Ther.*, 3:11-19, 1992; Breakfield et al., *Mol. Neurobiol.*, 1:337-371, 1987; Fresse et al., *Biochem. Pharmacol.*, 40:2189-2199, 1990), Sindbis viruses (Herweijer et al., *Human Gene Therapy*, 6:1161-1167, 1995; U.S. Pat. Nos. 5,091,309 and 5,221,879), alphaviruses (Schlesinger, *Trends Biotechnol.*, 11:18-22, 1993; Frolov et al., *Proc. Natl. Acad. Sci. USA*, 93:11371-11377, 1996) and retroviruses of avian (Brandopadhyay et al., *Mol. Cell Biol.*, 4:749-754,

1984; Petropoulos et al., *J. Virol.*, 66:3391-3397, 1992), murine (Miller, *Curr. Top. Microbiol. Immunol.*, 158:1-24, 1992; Miller et al., *Mol. Cell Biol.*, 5:431-437, 1985; Sorge et al., *Mol. Cell Biol.*, 4:1730-1737, 1984; Mann et al., *J. Virol.*, 54:401-407, 1985), and human origin (Page et al., *J. Virol.*, 64:5370-5276, 1990; Buchschalcher et al., *J. Virol.*, 66:2731-2739, 1992). Baculovirus (*Autographa californica* multi-nuclear polyhedrosis virus; AcMNPV) vectors are also known in the art, and may be obtained from commercial sources (such as PharMingen, San Diego, Calif.; Protein Sciences Corp., Meriden, Conn.; Stratagene, La Jolla, Calif.).

Viral vectors that encode one or more immunogenic TASA peptides typically include at least expression control element (e.g., a promoter) operationally linked to the nucleic acid sequence encoding the one or more immunogenic TASA peptides. The at least one expression control element is inserted in the poxviral vector to control and regulate the expression of the nucleic acid sequence. Examples of expression control elements of use in these vectors include, but are not limited to, lac system, operator and promoter regions of phage lambda, yeast promoters and promoters derived from polyoma, adenovirus, retrovirus or SV40. Additional operational elements include, but are not limited to, leader sequence, termination codons, polyadenylation signals and any other sequences necessary for the appropriate transcription and subsequent translation of the nucleic acid sequence encoding the one or more immunogenic TASA peptides in the host system. The expression vector can contain additional elements necessary for the transfer and subsequent replication of the expression vector containing the nucleic acid sequence in the host system. Examples of such elements include, but are not limited to, origins of replication and selectable markers. It will further be understood by one skilled in the art that such vectors are easily constructed using conventional methods (Ausubel et al., (1987) in "Current Protocols in Molecular Biology," John Wiley and Sons, New York, N.Y.) and are commercially available.

In one embodiment, a composition is provided that includes a recombinant virus comprising a vaccinia virus genome or portions thereof and a nucleic acid sequence encoding one or more immunogenic TASA peptides, and a recombinant virus comprising a nucleic acid sequence encoding an immunostimulatory molecule (for example, B 7-1 or B7-2). In such embodiments, any combination of encoding one or more immunogenic TASA peptides can be used, such as 2, 3, 4, 5, 6, 7 or more polynucleotides.

Isolation and purification of recombinantly expressed polypeptide can be carried out by conventional means including preparative chromatography and immunological separations. Once expressed, the one or more of the immunogenic TASA peptides can be purified according to standard procedures of the art, including ammonium sulfate precipitation, affinity columns, column chromatography, and the like (see, generally, R. Scopes, *Protein Purification*, Springer-Verlag, N. Y., 1982). Substantially pure compositions of at least about 90 to 95% homogeneity are disclosed herein, and 98 to 99% or more homogeneity can be used for pharmaceutical purposes. Once purified, partially or to homogeneity as desired, if to be used therapeutically, the polypeptides should be substantially free of endotoxin.

Therapeutic Methods and Pharmaceutical Compositions

The immunogenic TASA peptides disclosed herein (including a plurality of immunogenic peptides), or nucleic acids encoding the immunogenic TASA peptides (including a

plurality of nucleic acids), polynucleotides encoding such peptides and vectors comprising the polynucleotides, can be used in methods of generating an immune response, treating a subject with cancer and decreasing the growth of a tumor associated stromal cell, as described below. In several examples, the subject has a tumor or tumor microenvironment (TME) that expresses one or more TASAs.

In several embodiments, the methods include administering to a subject with a tumor a therapeutically effective amount of one or more of the immunogenic TASA peptides (for example, a plurality of immunogenic TASA peptides as described herein or one or more polynucleotides encoding these peptides), in order to generate an immune response.

The methods can include selecting a subject in need of treatment, such as a subject with a tumor, for example a tumor that expresses a TASA, or a TME that expresses a TASA. In several examples, the methods include selecting a subject with colorectal cancer or melanoma.

It is also disclosed herein that DLK1 protein, or a nucleic acid encoding DLK1 protein, can be used to treat a tumor and/or pathogenic angiogenesis. In several embodiments, the methods include administering to a subject with a tumor a therapeutically effective amount of one or more of the immunogenic DLK1 peptides (for example, a plurality of DLK1 peptides as described herein), one or more polynucleotides encoding these peptides, DLK1 protein, or a nucleic acid encoding DLK1, in order to generate an immune response. In some examples, the methods disclosed herein decrease pathological angiogenesis in the subject, to slow or inhibit the growth or metastasis of a tumor. In these applications, a therapeutically effective amount of a composition including the polypeptide, plurality of polypeptides, or polynucleotide is administered to a subject, thereby slowing or inhibiting the growth or the metastasis of a tumor, or other pathological angiogenesis, or to inhibit a sign or a symptom. Examples of suitable subjects include those diagnosed with or suspecting of having cancer (for example, a subject having a tumor), for example subjects having a carcinoma, such as a breast carcinoma, lung carcinoma, colorectal carcinoma, renal carcinoma, or melanoma. In additional examples, subject has a hematologic tumor, such as a hemangioma, lymphangioma, Kaposi sarcoma, or hemangioblastoma. In some examples, the tumor cells express DLK1. However, in some embodiments, the tumor cells do not express DLK1, but the pericytes in the blood vessels within the tumor express DLK1. In yet other examples, both the tumor cells and the pericytes in the blood vessels in the tumor express DLK1.

In some embodiments, compositions are administered to a subject having a disease such as cancer (for example, renal cell cancer), in an amount sufficient to reduce vascularization. Administration inhibits blood vessel growth, and/or normalizes the vasculature. Amounts effective for this use will depend upon the vascularization of the cancer, the general state of the patient's health, and the robustness of the patient's immune system. In one example, a therapeutically effective amount of the composition is that which provides either subjective relief of a symptom(s) or an objectively identifiable improvement, such as a decrease in vascularization, as noted by the clinician or other qualified observer. In some embodiments, these methods include administering to the subject one or more DLK polypeptides or DLK1 protein as disclosed herein.

In exemplary applications, compositions are administered to a subject having a disease, such as cancer (for example, colorectal cancer or melanoma), in an amount sufficient to raise an immune response to TASA-expressing cells. Administration induces a sufficient immune response to slow the

proliferation of such cells or to inhibit their growth, or to reduce a sign or a symptom of the tumor. Amounts effective for this use will depend upon the severity of the disease, the general state of the patient's health, and the robustness of the patient's immune system. In one example, a therapeutically effective amount of the compound is that which provides either subjective relief of a symptom(s) or an objectively identifiable improvement as noted by the clinician or other qualified observer.

One or more immunogenic TASA peptides or one or more polynucleotides encoding these peptides, DLK1 protein, or a polynucleotide encoding DLK1 protein can be administered by any means known to one of skill in the art (see Banga, A., "Parenteral Controlled Delivery of Therapeutic Peptides and Proteins," in *Therapeutic Peptides and Proteins*, Technomic Publishing Co., Inc., Lancaster, Pa., 1995) either locally or systemically, such as by intramuscular, subcutaneous, intraperitoneal or intravenous injection, but even oral, nasal, transdermal or anal administration is contemplated. In one embodiment, administration is by subcutaneous or intramuscular injection. To extend the time during which the peptide, protein or polynucleotide is available to stimulate a response, the peptide, protein or polynucleotide can be provided as an implant, an oily injection, or as a particulate system. The particulate system can be a microparticle, a microcapsule, a microsphere, a nanocapsule, or similar particle. (see, e.g., Banga, supra). A particulate carrier based on a synthetic polymer has been shown to act as an adjuvant to enhance the immune response, in addition to providing a controlled release. Aluminum salts can also be used as adjuvants to produce an immune response.

Optionally, one or more cytokines, such as IL-2, IL-6, IL-12, RANTES, GM-CSF, TNF- α , or IFN- γ , one or more growth factors, such as GM-CSF or G-CSF, one or more costimulatory molecules, such as ICAM-1, LFA-3, CD72, B7-1, B7-2, or other B7 related molecules; one or more molecules such as OX-40L or 41 BBL, or combinations of these molecules can be used as biological adjuvants (see, for example, Salgaller et al., 1998, *J. Surg. Oncol.* 68(2):122-38; Lotze et al., 2000, *Cancer J Sci. Am.* 6(Suppl 1):S61-6; Cao et al., 1998, *Stem Cells* 16(Suppl 1):251-60; Kuiper et al., 2000, *Adv. Exp. Med. Biol.* 465:381-90). These molecules can be administered systemically (or locally) to the host. In several examples, IL-2, RANTES, GM-CSF, TNF- α , IFN- γ , G-CSF, LFA-3, CD72, B7-1, B7-2, B7-1 B7-2, OX-40L, 41 BBL and ICAM-1 are administered.

In one specific, non-limiting example, one or more immunogenic TASA peptides (for example, a plurality of such peptides as described herein), or DLK1 protein, is administered in a manner to direct the immune response to a cellular response (that is, a cytotoxic T lymphocyte (CTL) response), rather than a humoral (antibody) response.

A number of means for inducing cellular responses, both in vitro and in vivo, are known. Lipids have been identified as agents capable of assisting in priming CTL in vivo against various antigens. For example, as described in U.S. Pat. No. 5,662,907, palmitic acid residues can be attached to the alpha and epsilon amino groups of a lysine residue and then linked (for example, via one or more linking residues, such as glycine, glycine-glycine, serine, serine-serine, or the like) to an immunogenic peptide. The lipidated peptide can then be injected directly in a micellar form, incorporated in a liposome, or emulsified in an adjuvant. As another example, *E. coli* lipoproteins, such as tripalmitoyl-S-glycerylcysteinyl-serine can be used to prime tumor specific CTL when covalently attached to an appropriate peptide (see, Deres et al., *Nature* 342:561, 1989). Further, as the induction of neu-

tralizing antibodies can also be primed with the same molecule conjugated to a peptide which displays an appropriate epitope, two compositions can be combined to elicit both humoral and cell-mediated responses where that is deemed desirable.

In yet another embodiment, to induce a CTL response to one or more immunogenic TASA peptides, a MHC Class II-restricted T-helper epitope is added to the one or more immunogenic TASA peptides to induce T-helper cells to secrete cytokines in the microenvironment to activate CTL precursor cells. The technique further involves adding short lipid molecules to retain the construct at the site of the injection for several days to localize the antigen at the site of the injection and enhance its proximity to dendritic cells or other "professional" antigen presenting cells over a period of time (see Chesnut et al., "Design and Testing of Peptide-Based Cytotoxic T-Cell-Mediated Immunotherapeutics to Treat Infectious Diseases and Cancer," in Powell et al., eds., *Vaccine Design, the Subunit and Adjuvant Approach*, Plenum Press, New York, 1995).

A pharmaceutical composition including one or more immunogenic TASA peptides or DLK1 protein is provided. In some examples, the composition includes a plurality of immunogenic TASA peptides as described herein. These compositions are used to generate an immune response, such as for immunotherapy. In one embodiment, one or more immunogenic TASA peptides are mixed with an adjuvant containing two or more of a stabilizing detergent, a micelle-forming agent, and an oil. Suitable stabilizing detergents, micelle-forming agents, and oils are detailed in U.S. Pat. No. 5,585,103; U.S. Pat. No. 5,709,860; U.S. Pat. No. 5,270,202; and U.S. Pat. No. 5,695,770, all of which are incorporated by reference. A stabilizing detergent is any detergent that allows the components of the emulsion to remain as a stable emulsion. Such detergents include polysorbate, 80 (TWEEN) (Sorbitan-mono-9-octadecenoate-poly(oxy-1,2-ethanediyl; manufactured by ICI Americas, Wilmington, Del.), TWEEN 40TM, TWEEN 20TM, TWEEN 60TM, ZwittergentTM 3-12, TEEPOL HB7TM, and SPAN 85TM. These detergents are usually provided in an amount of approximately 0.05 to 0.5%, such as at about 0.2%. A micelle forming agent is an agent which is able to stabilize the emulsion formed with the other components such that a micelle-like structure is formed. Such agents generally cause some irritation at the site of injection in order to recruit macrophages to enhance the cellular response. Examples of such agents include polymer surfactants described by BASF Wyandotte publications, e.g., Schmolka, *J. Am. Oil. Chem. Soc.* 54:110, 1977, and Hunter et al., *J. Immunol.* 129:1244, 1981, PLURONICTM L62LF, L101, and L64, PEG1000, and TETRONICTM 1501, 150R1, 701, 901, 1301, and 130R1. The chemical structures of such agents are well known in the art. In one embodiment, the agent is chosen to have a hydrophile-lipophile balance (HLB) of between 0 and 2, as defined by Hunter and Bennett, *J. Immun.* 133:3167, 1984. The agent can be provided in an effective amount, for example between 0.5 and 10%, or in an amount between 1.25 and 5%.

The oil included in the composition is chosen to promote the retention of the antigen in oil-in-water emulsion, such as to provide a vehicle for the desired antigen, and preferably has a melting temperature of less than 65° C. such that emulsion is formed either at room temperature (about 20° C. to 25° C.), or once the temperature of the emulsion is brought down to room temperature. Examples of such oils include squalene, Squalane, EICOSANETM, tetratetracontane, glycerol, and peanut oil or other vegetable oils. In one specific, non-limiting example, the oil is provided in an amount between 1 and

10%, or between 2.5 and 5%. The oil should be both biodegradable and biocompatible so that the body can break down the oil over time, and so that no adverse effects, such as granulomas, are evident upon use of the oil.

In one embodiment, the adjuvant is a mixture of stabilizing detergents, micelle-forming agent, and oil available under the name PROVAX® (IDEC Pharmaceuticals, San Diego, Calif.). An adjuvant can also be an immunostimulatory nucleic acid, such as a nucleic acid including a CpG motif, or a biological adjuvant (see above).

Controlled release parenteral formulations can be made as implants, oily injections, or as particulate systems. For a broad overview of protein delivery systems, see Banga, *Therapeutic Peptides and Proteins: Formulation, Processing, and Delivery Systems*, Technomic Publishing Company, Inc., Lancaster, Pa., 1995. Particulate systems include microspheres, microparticles, microcapsules, nanocapsules, nanospheres, and nanoparticles. Microcapsules contain the therapeutic protein as a central core. In microspheres, the therapeutic agent is dispersed throughout the particle. Particles, microspheres, and microcapsules smaller than about 1 μ m are generally referred to as nanoparticles, nanospheres, and nanocapsules, respectively. Capillaries have a diameter of approximately 5 μ m so that only nanoparticles are administered intravenously. Microparticles are typically around 100 μ m in diameter and are administered subcutaneously or intramuscularly (see Kreuter, *Colloidal Drug Delivery Systems*, J. Kreuter, ed., Marcel Dekker, Inc., New York, N.Y., pp. 219-342, 1994; Tice & Tabibi, *Treatise on Controlled Drug Delivery*, A. Kydonieus, ed., Marcel Dekker, Inc. New York, N.Y., pp. 315-339, 1992).

Polymers can be used for ion-controlled release. Various degradable and nondegradable polymeric matrices for use in controlled drug delivery are known in the art (Langer, *Accounts Chem. Res.* 26:537, 1993). For example, the block copolymer, polaxamer 407 exists as a viscous yet mobile liquid at low temperatures but forms a semisolid gel at body temperature. It has shown to be an effective vehicle for formulation and sustained delivery of recombinant interleukin-2 and urease (Johnston et al., *Pharm. Res.* 9:425, 1992; and Pec, *J. Parent. Sci. Tech.* 44(2):58, 1990). Alternatively, hydroxyapatite has been used as a microcarrier for controlled release of proteins (Ijntema et al., *Int. J. Pharm.* 112:215, 1994). In yet another aspect, liposomes are used for controlled release as well as drug targeting of the lipid-capsulated drug (Betageri et al., *Liposome Drug Delivery Systems*, Technomic Publishing Co., Inc., Lancaster, Pa., 1993). Numerous additional systems for controlled delivery of therapeutic proteins are known (e.g., U.S. Pat. No. 5,055,303; U.S. Pat. No. 5,188,837; U.S. Pat. No. 4,235,871; U.S. Pat. No. 4,501,728; U.S. Pat. No. 4,837,028; U.S. Pat. No. 4,957,735; and U.S. Pat. No. 5,019,369; U.S. Pat. No. 5,055,303; U.S. Pat. No. 5,514,670; U.S. Pat. No. 5,413,797; U.S. Pat. No. 5,268,164; U.S. Pat. No. 5,004,697; U.S. Pat. No. 4,902,505; U.S. Pat. No. 5,506,206; U.S. Pat. No. 5,271,961; U.S. Pat. No. 5,254,342; and U.S. Pat. No. 5,534,496).

In another embodiment, a pharmaceutical composition including one or more polynucleotides encoding one or more immunogenic TASA peptides, or encoding DLK1 protein, is provided. For example the composition can include one or more polynucleotides encoding a plurality of immunogenic TASA peptides as described herein. A therapeutically effective amount of polynucleotide can be administered to a subject in order to generate an immune response. In one specific, non-limiting example, a therapeutically effective amount of the polynucleotide is administered to a subject to treat colorectal cancer, hepatocellular carcinoma or melanoma.

Optionally, one or more cytokines, such as IL-2, IL-6, IL-12, RANTES, GM-CSF, TNF- α , or IFN- γ , one or more growth factors, such as GM-CSF or G-CSF, one or more costimulatory molecules, such as ICAM-1, LFA-3, CD72, B7-1, B7-2, or other B7 related molecules; one or more molecules such as OX-40L or 41 BBL, or combinations of these molecules, can be used as biological adjuvants (see, for example, Salgaller et al., 1998, *J. Surg. Oncol.* 68(2):122-38; Lotze et al., 2000, *Cancer J Sci. Am.* 6(Suppl 1):561-6; Cao et al., 1998, *Stem Cells* 16(Suppl 1):251-60; Kuiper et al., 2000, *Adv. Exp. Med. Biol.* 465:381-90). These molecules can be administered systemically to the host. It should be noted that these molecules can be co-administered via insertion of a nucleic acid encoding the molecules into a vector, for example, a viral vector. In various embodiments, the nucleic acid encoding the biological adjuvant can be cloned into same vector as an immunogenic TASA peptide coding sequence, or the nucleic acid can be cloned into one or more separate vectors for co-administration. In addition, nonspecific immunomodulating factors such as Bacillus Calmette-Guerin (BCG) and levamisole can be co-administered.

One approach to administration of nucleic acids is direct immunization with plasmid DNA, such as with a mammalian expression plasmid. As described above, nucleotide sequence encoding immunogenic TASA peptides, or encoding DLK1 protein, can be placed under the control of a promoter to increase expression of the molecule.

Immunization by nucleic acid constructs is well known in the art and taught, for example, in U.S. Pat. No. 5,643,578 (which describes methods of immunizing vertebrates by introducing DNA encoding a desired antigen to elicit a cell-mediated or a humoral response), and U.S. Pat. No. 5,593,972 and U.S. Pat. No. 5,817,637 (which describe operably linking a nucleic acid sequence encoding an antigen to regulatory sequences enabling expression). U.S. Pat. No. 5,880,103 describes several methods of delivery of nucleic acids encoding immunogenic peptides or other antigens to an organism. The methods include liposomal delivery of the nucleic acids (or of the synthetic peptides themselves), and immune-stimulating constructs, or ISCOMS™, negatively charged cage-like structures of 30-40 nm in size formed spontaneously on mixing cholesterol and Quil A™ (saponin). Protective immunity has been generated in a variety of experimental models of infection, including toxoplasmosis and Epstein-Barr virus-induced tumors, using ISCOMS™ as the delivery vehicle for antigens (Mowat and Donachie, *Immunol. Today* 12:383, 1991). Doses of antigen as low as 1 μ g encapsulated in ISCOMS™ have been found to produce Class I mediated CTL responses (Takahashi et al., *Nature* 344:873, 1990).

In another approach to using nucleic acids for immunization, one or more immunogenic TASA peptides, or DLK1 protein, can also be expressed by attenuated viral hosts or vectors or bacterial vectors. Recombinant vaccinia virus, poxvirus, adeno-associated virus (AAV), herpes virus, retrovirus, or other viral vectors can be used to express one or more TASA peptides, thereby eliciting a CTL response. For example, vaccinia vectors and methods useful in immunization protocols are described in U.S. Pat. No. 4,722,848. BCG (Bacillus Calmette Guerin) provides another vector for expression of the peptides (see Stover, *Nature* 351:456-460, 1991).

A first recombinant virus, such as a poxvirus (for example, vaccinia virus) encoding one or more TASA immunogenic polypeptides can be used in conjunction with a second recombinant virus which has incorporated into a viral genome or infectable portion thereof one or more genes or DNA sequences encoding B7-1, B7-2, or B7-1 and B7-2, wherein

the composition is able to coinfect a host cell resulting in coexpression of the polypeptide and the B7-1, B7-2, or B7-1 and B7-2 encoding genes or DNA sequences (see U.S. Pat. No. 6,893,869, and U.S. Pat. No. 6,045,908, which are incorporated by reference herein).

When a viral vector is utilized, it is desirable to provide the recipient with a dosage of each recombinant virus in the composition in the range of from about 10^5 to about 10^{10} plaque forming units/mg mammal, although a lower or higher dose can be administered. The composition of recombinant viral vectors can be introduced into a mammal either prior to any evidence of a cancer, or to mediate regression of the disease in a mammal afflicted with the cancer. Examples of methods for administering the composition into mammals include, but are not limited to, exposure of cells to the recombinant virus *ex vivo*, or injection of the composition into the affected tissue or intravenous, subcutaneous, intradermal or intramuscular administration of the virus. Alternatively the recombinant viral vector or combination of recombinant viral vectors may be administered locally by direct injection into the cancerous lesion in a pharmaceutically acceptable carrier. Generally, the quantity of recombinant viral vector, carrying the nucleic acid sequence of one or more immunogenic TASA peptides (or DLK1 protein) to be administered is based on the titer of virus particles. An exemplary range of the immunogen to be administered is 10^5 to 10^{10} virus particles per mammal, such as a human.

In one embodiment the recombinant viruses have been constructed to express cytokines (such as TNF- α , IL-6, GM-CSF, and IL-2), and co-stimulatory and accessory molecules (B7-1, B7-2) alone and in a variety of combinations. Simultaneous production of an immunostimulatory molecule and one or more immunogenic TASA peptides (or DLK1 protein) enhances the immune response. Without being bound by theory, dependent upon the specific immunostimulatory molecules, different mechanisms might be responsible for the enhanced immunogenicity: augmentation of help signal (IL-2), recruitment of professional APC (GM-CSF), increase in CTL frequency (IL-2), effect on antigen processing pathway and MHC expression (IFN γ and TNF α) and the like. For example, IL-2, IL-6, interferon, tumor necrosis factor, or a nucleic acid encoding these molecules, can be administered in conjunction with one or more TASA immunogenic polypeptides, a nucleic acid encoding one or more immunogenic TASA peptides, DLK1 protein or a nucleic acid encoding DLK1 protein. The co-expression of one or more immunogenic TASA peptides, DLK1 protein or a nucleic acid encoding DLK1 protein, together with at least one immunostimulatory molecule can be effective in an animal model to show anti-tumor effects.

In one embodiment, a nucleic acid encoding one or more immunogenic TASA peptides (or DLK1 protein) is introduced directly into cells. For example, the nucleic acid can be loaded onto gold microspheres by standard methods and introduced into the skin by a device such as Bio-Rad's HELIOSTM Gene Gun. The nucleic acids can be "naked," consisting of plasmids under control of a strong promoter. Typically, the DNA is injected into muscle, although it can also be injected directly into other sites, including tissues in proximity to metastases. Dosages for injection are usually around 0.5 μ g/kg to about 50 mg/kg, and typically are about 0.005 mg/kg to about 5 mg/kg (see, for example, U.S. Pat. No. 5,589,466).

In one specific, non-limiting example, a pharmaceutical composition for intravenous administration would include about 0.1 μ g to 10 mg of one or more immunogenic TASA peptides (or DLK1 protein) per patient per day. Dosages from

0.1 up to about 100 mg per patient per day can be used, particularly if the agent is administered to a secluded site and not into the circulatory or lymph system, such as into a body cavity or into a lumen of an organ. Actual methods for preparing administrable compositions are known or apparent to those skilled in the art and are described in more detail in such publications as *Remington's Pharmaceutical Sciences*, 19th Ed., Mack Publishing Company, Easton, Pa., 1995.

Single or multiple administrations of the compositions are administered depending on the dosage and frequency as required and tolerated by the subject. In one embodiment, the dosage is administered once as a bolus, but in another embodiment can be applied periodically until a therapeutic result is achieved. Generally, the dose is sufficient to treat or ameliorate symptoms or signs of disease without producing unacceptable toxicity to the subject. Systemic or local administration can be utilized.

In another method, antigen presenting cells (APCs), such as dendritic cells, are pulsed or co-incubated with peptides comprising one or more immunogenic TASA peptides, or with DLK1 protein, or a nucleic acid encoding the peptide(s) or protein, *in vitro*. In one specific, non-limiting example, the antigen presenting cells can be autologous cells. A therapeutically effective amount of the antigen presenting cells can then be administered to a subject.

One or more immunogenic TASA peptides or DLK1 protein, or a nucleic acid encoding the peptide(s) or protein, can be delivered to the dendritic cells or to dendritic cell precursors via any method known in the art, including, but not limited to, pulsing dendritic cells directly with antigen, or utilizing a broad variety of antigen delivery vehicles, such as, for example, liposomes, or other vectors known to deliver antigen to cells. In one specific, non-limiting example an antigenic formulation includes about 0.1 μ g to about 1,000 μ g, or about 1 to about 100 μ g of one or more immunogenic TASA peptides. One or more immunogenic TASA peptides (or DLK1 protein), or a nucleic acid encoding the peptide(s) or protein, can also be administered with agents that promote dendritic cell maturation. Specific, non-limiting examples of agents of use are interleukin-4 (IL-4) and granulocyte/macrophage colony stimulating factor (GM-CSF), or flt-3 ligand (flt-3L). The preparation can also contain buffers, excipients, and preservatives, amongst other ingredients.

In one embodiment, mature antigen presenting cells are generated to present one or more immunogenic TASA peptides, such as DLK1 peptides. These dendritic cells are then administered alone (or in combination with another agent) to a subject with a tumor, for example a tumor that expresses the corresponding TASA, such as a colorectal tumor or melanoma.

Alternatively, the APCs are used to sensitize CD8 cells, such as tumor infiltrating lymphocytes (TILs) from tumors or peripheral blood lymphocytes (PBLs). The TILs or PBLs can be from the same subject (autologous) that is to be treated. Alternatively, the TILs or PBLs can be heterologous. However, they should at least be MHC Class-I restricted to the HLA types the subject possesses. An effective amount of the sensitized cells are then administered to the subject.

Peripheral blood mononuclear cells (PBMCs) can be used as the responder cell source of CTL precursors. The appropriate antigen-presenting cells are incubated with peptide, after which the peptide-loaded antigen-presenting cells are then incubated with the responder cell population under optimized culture conditions. Positive CTL activation can be determined by assaying the culture for the presence of CTLs that kill radio-labeled target cells, both specific peptide-

pulsed targets as well as target cells expressing endogenously processed forms of the antigen from which the peptide sequence was derived.

The cells can be administered to a subject to inhibit the growth of TASA expressing cells in a tumor or TME. In these applications, a therapeutically effective amount of activated antigen presenting cells, or activated lymphocytes, are administered to a subject suffering from a disease, in an amount sufficient to raise an immune response to TASA expressing cells. The resulting immune response is sufficient to slow the proliferation of such cells or to inhibit their growth, or to reduce a sign or a symptom of the tumor.

In a supplemental method, any of these immunotherapies is augmented by administering a cytokine, such as interleukin (IL)-2, IL-3, IL-6, IL-10, IL-12, IL-15, GM-CSF, or interferons.

The methods of treating a subject with a tumor described herein can be accompanied by administration of anti-cancer or anti-angiogenesis agents or therapeutic treatments (such as surgical resection of a tumor or radiation therapy). For example, the subject can receive additional therapies (a) prior to, during, or following administration of a therapeutic amount of one or more immunogenic TASA peptides, or (b) prior to, during, or following administration of a therapeutic amount of DLK1 protein or a nucleic acid encoding DLK1 protein. In one example, the subject receives one or more treatments to remove or reduce the tumor prior to administration of a therapeutic amount of one or more agents for treatment of the tumor. For example, the additional agent may include, but is not limited to, a chemotherapeutic agent, an anti-angiogenic agent, or a combination thereof. In another example, at least part of the tumor is surgically or otherwise excised or reduced in size or volume prior to administering the therapeutically effective amount of the antibody or conjugate. In some embodiments, the chemotherapeutic agent reduces suppressor cells in the tumor microenvironment or fosters the recruitment of vaccine-induced T cells into the tumor site. In some examples, the agent is bevacizumab, sunitinib, axitinib, HSP90 inhibitors, or gencitabine/fludarabine.

Particular examples of additional therapeutic agents that can be used include microtubule binding agents, DNA intercalators or cross-linkers, DNA synthesis inhibitors, DNA and/or RNA transcription inhibitors, antibodies, enzymes, enzyme inhibitors, gene regulators, angiogenesis inhibitors. These agents (which are administered at a therapeutically effective amount) and treatments can be used alone or in combination. For example, any suitable anti-cancer or anti-angiogenic agent can be administered in combination with the immunogenic TASA peptides or DLK1 protein disclosed herein, or polynucleotides encoding such peptides or protein and viral vectors include these polynucleotides. Methods and therapeutic dosages of such agents are known to those skilled in the art, and can be determined by a skilled clinician.

Microtubule binding agent refers to an agent that interacts with tubulin to stabilize or destabilize microtubule formation thereby inhibiting cell division. Examples of microtubule binding agents that can be used in conjunction with the disclosed therapy include, without limitation, paclitaxel, docetaxel, vinblastine, vindesine, vinorelbine (navelbine), the epothilones, colchicine, dolastatin 15, nocodazole, podophyllotoxin and rhizoxin. Analogs and derivatives of such compounds also can be used and are known to those of ordinary skill in the art. For example, suitable epothilones and epothilone analogs are described in International Publication No. WO 2004/018478. Taxoids, such as paclitaxel and doc-

etaxel, as well as the analogs of paclitaxel taught by U.S. Pat. Nos. 6,610,860; 5,530,020; and 5,912,264 can be used.

Suitable DNA and/or RNA transcription regulators, including, without limitation, actinomycin D, daunorubicin, doxorubicin and derivatives and analogs thereof also are suitable for use in combination with the disclosed therapies. DNA intercalators and cross-linking agents that can be administered to a subject include, without limitation, cisplatin, carboplatin, oxaliplatin, mitomycins, such as mitomycin C, bleomycin, chlorambucil, cyclophosphamide and derivatives and analogs thereof. DNA synthesis inhibitors suitable for use as therapeutic agents include, without limitation, methotrexate, 5-fluoro-5'-deoxyuridine, 5-fluorouracil and analogs thereof. Examples of suitable enzyme inhibitors include, without limitation, camptothecin, etoposide, formestane, trichostatin and derivatives and analogs thereof. Suitable compounds that affect gene regulation include agents that result in increased or decreased expression of one or more genes, such as raloxifene, 5-azacytidine, 5-aza-2'-deoxycytidine, tamoxifen, 4-hydroxytamoxifen, mifepristone and derivatives and analogs thereof.

Examples of the commonly used chemotherapy drugs include Adriamycin, Alkeran, Ara-C, BiCNU, Busulfan, CCNU, Carboplatinum, Cisplatinum, Cytosan, Daunorubicin, DTIC, 5-FU, Fludarabine, Hydrea, Idarubicin, Ifosfamide, Methotrexate, Mithramycin, Mitomycin, Mitoxantrone, Nitrogen Mustard, Taxol (or other taxanes, such as docetaxel), Velban, Vincristine, VP-16, while some more newer drugs include Gemcitabine (Gemzar), Herceptin, Irinotecan (Camptosar, CPT-11), Leustatin, Navelbine, Rituxan STI-571, Taxotere, Topotecan (Hycamtin), Xeloda (Capecitabine), Zevelin and calcitriol.

Non-limiting examples of immunomodulators that can be used include AS-101 (Wyeth-Ayerst Labs.), bropirimine (Upjohn), gamma interferon (Genentech), GM-CSF (granulocyte macrophage colony stimulating factor; Genetics Institute), IL-2 (Cetus or Hoffman-LaRoche), human immune globulin (Cutter Biological), IMREG (from Imreg of New Orleans, La.), SK&F 106528, and TNF (tumor necrosis factor; Genentech).

Non-limiting examples of anti-angiogenic agents include molecules, such as proteins, enzymes, polysaccharides, oligonucleotides, DNA, RNA, and recombinant vectors, and small molecules that function to reduce or even inhibit blood vessel growth. Examples of suitable angiogenesis inhibitors include, without limitation, angiostatin K1-3, staurosporine, genistein, fumagillin, medroxyprogesterone, suramin, interferon-alpha, metalloproteinase inhibitors, platelet factor 4, somatostatin, thrombospondin, endostatin, thalidomide, and derivatives and analogs thereof. For example, in some embodiments the anti-angiogenesis agent is an antibody that specifically binds to VEGF (e.g., Avastin, Roche) or a VEGF receptor (e.g., a VEGFR2 antibody). In one example the anti-angiogenic agent includes a VEGFR2 antibody, or DMXAA (also known as Vadimezan or ASA404; available commercially, e.g., from Sigma Corp., St. Louis, Mo.) or both. The anti-angiogenic agent can be bevacizumab, sunitinib, an anti-angiogenic tyrosine kinase inhibitors (TKI), such as sunitinib, xitinib and dasatinib. These can be used individually or in any combination.

Exemplary kinase inhibitors include Gleevec, Iressa, and Tarceva, sunitinib, sorafenib, anitinib, and dasatinib that prevent phosphorylation and activation of growth factors. Antibodies that can be used include Herceptin and Avastin that block growth factors and the angiogenic pathway. These can be used individually or in combination.

In some examples, the additional agent is a monoclonal antibody, for example, 3F8, Abagovomab, Adecatumumab, Afutuzumab, Alacizumab, Alemtuzumab, Altumomab pentetate, Anatumomab mafenatox, Apolizumab, Arcitumomab, Bavtuzumab, Bectumomab, Belimumab, Besilesomab, Bevacizumab, Bivatuzumab mertansine, Blinatumomab, Brentuximab vedotin, Cantuzumab mertansine, Capromab pendetide, Catumaxomab, CC49, Cetuximab, Citatuzumab bogatox, Cixutumumab, Clivatuzumab tetraxetan, Conatumumab, Dacetuzumab, Detumomab, Ecomeximab, Eculizumab, Edrecolomab, Epratuzumab, Ertumaxomab, Etaracizumab, Farletuzumab, Figitumumab, Galiximab, Gemtuzumab ozogamicin, Girentuximab, Glembatumumab vedotin, Ibritumomab tiuxetan, Igovomab, Imciromab, Intetumumab, Inotuzumab ozogamicin, Ipilimumab, Iratumumab, Labetuzumab, Lexatumumab, Lintuzumab, Lorvotuzumab mertansine, Lucatumumab, Lumiliximab, Mapatumumab, Matuzumab, Mepolizumab, Metelimumab, Milatuzumab, Mitumomab, Morolimumab, Nacolomab tafenoate, Naptumomab estafenatox, Necitumumab, Nimotuzumab, Nofetumomab merpentan, Ofatumumab, Olaratumab, Oporetuzumab monatox, Oregovomab, Panitumumab, Pentumomab, Pertuzumab, Pintumomab, Pritumumab, Ramucirumab, Rilotumumab, Rituximab, Robatumumab, Satumomab pendetide, Sibrotuzumab, Sonepcizumab, Tacatuzumab tetraxetan, Taplitumomab paptax, Tenatumomab, TGN1412, Ticilimumab (tremelimumab), Tigatuzumab, TNX-650, Trastuzumab, Tremelimumab, Tucotuzumab celmoleukin, Veltuzumab, Volociximab, Votumumab, Zalutumumab.

Another common treatment for some types of cancer is surgical treatment, for example surgical resection of the cancer or a portion of it. Another example of a treatment is radiotherapy, for example administration of radioactive material or energy (such as external beam therapy) to the tumor site to help eradicate the tumor or shrink it prior to surgical resection.

Other therapeutic agents, for example anti-tumor agents, that may or may not fall under one or more of the classifications above, also are suitable for administration in combination with the disclosed therapies. By way of example, such agents include adriamycin, apigenin, rapamycin, zebularine, cimetidine, and derivatives and analogs thereof. Further examples include one or more additional vaccines targeting tumor antigens or tumor stem cells (such as a tumor initiating cell). The skilled artisan is familiar with such vaccines.

Reagents for the Detection of CD8⁺ cells that Specifically Bind TASAs

Reagents are provided herein for the detection of CD8 expressing cells that specifically bind the TASAs described herein. These reagents are tetrameric MHC Class I/immunogenic TASA peptide complexes. These tetrameric complexes include an immunogenic TASA peptide that includes at most twelve consecutive amino acids, wherein the isolated polypeptide comprises the amino acid sequence as shown in Table 1. Specific examples of immunogenic TASA peptides that are nine or ten amino acids in length are disclosed above.

Tetrameric MHC Class I/peptide complexes can be synthesized using methods well known in the art (Altmann et al., *Science* 274:94, 1996, which is herein incorporated by reference). In one specific non-limiting example, purified HLA heavy chain and β 2-microglobulin (β 2m) can be synthesized by means of a prokaryotic expression system. One specific, non-limiting example of an expression system of use is the pET system (R&D Systems, Minneapolis, Minn.). The heavy

chain is modified by deletion of the trans-membrane and cytosolic tail and COOH-terminal addition of a sequence containing the biotin protein ligase (Bir-A) enzymatic biotinylation site. Heavy chain, β 2m, and peptide are then refolded. The refolded product can be isolated by any means known in the art, and then biotinylated by Bir-A. A tetramer is then produced by contacting the biotinylated product with streptavidin.

In one embodiment, the streptavidin is labeled. Suitable labels include, but are not limited to, enzymes, magnetic beads, colloidal magnetic beads, haptens, fluorochromes, metal compounds, radioactive compounds or drugs. The enzymes that can be conjugated to streptavidin include, but are not limited to, alkaline phosphatase, peroxidase, urease and β -galactosidase. The fluorochromes that can be conjugated to the streptavidin include, but are not limited to, fluorescein isothiocyanate, tetramethylrhodamine isothiocyanate, phycoerythrin, allophycocyanins and Texas Red. For additional fluorochromes that can be conjugated to streptavidin, see Haugland, R. P., *Molecular Probes: Handbook of Fluorescent Probes and Research Chemicals* (1992-1994). The metal compounds that can be conjugated to the streptavidin include, but are not limited to, ferritin, colloidal gold, and particularly, colloidal superparamagnetic beads. The haptens that can be conjugated to the streptavidin include, but are not limited to, biotin, digoxigenin, oxazalone, and nitrophenol. The radioactive compounds that can be conjugated to streptavidin are known to the art, and include but are not limited to technetium 99m (^{99}Tc), ^{125}I and amino acids comprising any radionuclides, including, but not limited to, ^{14}C , ^3H and ^{35}S . Generally, streptavidin labeled with a fluorochrome is utilized in the methods disclosed herein.

In one embodiment, suspension of cells including T cells that specifically recognize one or more TASAs is produced, and the cells are reacted with the tetramer in suspension. In one embodiment, these reagents are used to label cells, which are then analyzed by fluorescence activated cell sorting (FACS). A machine for FACS employs a plurality of color channels, low angle and obtuse light-scattering detection channels, and impedance channels, among other more sophisticated levels of detection, to separate or sort cells. Any FACS technique can be employed as long as it is not detrimental to the detection of the desired cells. (For exemplary methods of FACS see U.S. Pat. No. 5,061,620.)

EXAMPLES

The following examples are provided to illustrate certain particular features and/or embodiments and should not be construed as limiting.

Example 1

Intratumoral Gene Therapy Induces Cross-Priming of T Cells Reactive Against Tumor-Associated Stromal Antigens

This example illustrates that cross-priming of CD8⁺ T cells reactive against TASA is a general paradigm for effective immunotherapy. The results show that protective CD8⁺ T cells induced as a consequence of effective intratumoral DC/IL12 therapy recognize both tumor-associated stromal cells (i.e. flow-sorted pericytes and VEC) and naturally-processed and HLA-A2-presented peptides derived from TASA. These data illustrate the therapeutic targeting of TASA (via intratumoral cytokine gene therapy or specific vaccination) as a means to treat vascularized solid tumors.

Materials and Methods

Mice.

HHD mice fail to express H-2^b class I molecules, with their cells instead expressing an HLA-A*0201-hβ2 microglobulin single-chain (HHD) gene product (Firat et al., *Int Immunol.*, 14:925-934, 2002). Ag-specific CD8⁺ T cell responses in HHD mice recapitulate those observed in HLA-A2⁺ human donors (Firat et al., *Int Immunol.*, 14:925-934, 2002). Female 6-8 week old mice were used in all experiments and were handled in accordance with an Institutional Animal Care and Use Committee (IACUC)-approved protocol. HLA-A2 expression on peripheral blood cells isolated from HHD mice via tail venipuncture was confirmed by coordinate positive staining as assessed by flow cytometry using two monoclonal antibodies (mAbs) MA2.1 (reactive against HLA-A2 and HLA-B17) and BB7.2 (reactive against HLA-A2 and HLA-Aw69) (both monoclonal antibodies from the American Type Culture collection; ATCC, Manassas, Va.).

B-cell hybridoma (Tatsumi et al., *Cancer Res.*; 63:4481-4489, 2003). Cell lines were free of mycoplasma contamination and were maintained in CM (RPMI 1640 supplemented with 10% heat-inactivated fetal bovine serum, 100 U/ml penicillin, 100 µg/ml streptomycin, and 10 mM L-glutamine (all reagents from Life Technologies, Inc., Grand Island, N.Y.)) in a humidified incubator at 5% CO₂ and 37° C.

RT-PCR.

Reverse transcriptase-PCR (RT-PCR) was performed using the primer pairs shown in Table 2. Cycling times and temperatures were as follows: initial denaturation at 94° C. for 2 min (1 cycle), denaturation at 94° C. for 30 sec, annealing at 60° C. for 30 sec and elongation at 72° C. for 1 min (30 cycles), final extension at 72° C. for 5 min (1 cycle). PCR products were identified by image analysis software for gel documentation (LabWorks 4.6 Software; UVP, Upland, Calif.) following electrophoresis on 1.2% agarose gels and staining with ethidium bromide (Sigma-Aldrich).

TABLE 2

RT-PCR primers.		
Target	RT-PCR primers	Product (bp)
CD31	Forward 5'-3': AGCCCAACCAGACATGGAA (SEQ ID NO: 33) Reverse 5'-3': CTGGCTCTGTTGGAGGCTGT (SEQ ID NO: 34)	337
DLK1	Forward 5'-3': CTGCACACCTGGGTTCTCTG (SEQ ID NO: 35) Reverse 5'-3': GCATGGGTAGGGGTACAGC (SEQ ID NO: 36)	202
EphA2	Forward 5'-3': GGGGATGCCAACAGCTATAA (SEQ ID NO: 37) Reverse 5'-3': CTCCTGCCAGTACCAGAAGC (SEQ ID NO: 38)	232
gp100	Forward 5'-3': CATCAATGGGAGCCAGGTGT (SEQ ID NO: 39) Reverse 5'-3': TGAAGGTTGAAGTGGCGTGA (SEQ ID NO: 40)	296
HBB	Forward 5'-3': TCAGAAACAGACATCATGGTGC (SEQ ID NO: 41) Reverse 5'-3': TAGACAAATAGCAGAAAAGGGGC (SEQ ID NO: 42)	480
NG2	Forward 5'-3': ACAGACGCCTTTGTTCTGCT (SEQ ID NO: 43) Reverse 5'-3': TCGGAAGAAATGTCCAGGAG (SEQ ID NO: 44)	399
NRP1	Forward 5'-3': TCCAAGTGGACCTGGGAGAT (SEQ ID NO: 45) Reverse 5'-3': TTCACAGCCCAGTAGCTCCA (SEQ ID NO: 46)	299
NRP2	Forward 5'-3': CCGGAAGAGACCTGTGGTTG (SEQ ID NO: 47) Reverse 5'-3': CCGATCGTCCCTTCCCTATC (SEQ ID NO: 48)	394
PDGFRβ	Forward 5'-3': TGCTCCTGGAGAGGCTTCTG (SEQ ID NO: 49) Reverse 5'-3': GGAGGAAGTGTGACTTCATTG (SEQ ID NO: 50)	301
PSMA	Forward 5'-3': CCTGCGGTGAAGTCTATCC (SEQ ID NO: 51) Reverse 5'-3': GTTTCAGCAAAGCCAGGTC (SEQ ID NO: 52)	300
RGS5	Forward 5'-3': AAGTTGGGAATTCTCCTCCAG (SEQ ID NO: 53) Reverse 5'-3': TTCCTCACTGAATTGAGACTTC (SEQ ID NO: 54)	203
TEM1	Forward 5'-3': TTCACCAACTGGGCCAGC (SEQ ID NO: 55) Reverse 5'-3': GTTGACACACATCTGCTGGC (SEQ ID NO: 56)	645
VEGFR1	Forward 5'-3': CCAACTACCTCAAGAGCAAAC (SEQ ID NO: 57) Reverse 5'-3': CCAGGTCCCGATGAATGCAC (SEQ ID NO: 58)	318
VEGFR2	Forward 5'-3': ACAGACAGTGGGATGGTCC (SEQ ID NO: 59) Reverse 5'-3': AAACAGGAGGTGAGCGCAG (SEQ ID NO: 60)	271
β-actin	Forward 5'-3': GGCATCGTGATGGACTCCG (SEQ ID NO: 61) Reverse 5'-3': GCTGGAAGGTGGACAGCGA (SEQ ID NO: 62)	615

Cell Lines and Culture.

B16 is an HLA-A2^{neg}, mMART-1⁺, mgp100⁺ melanoma cell line (syngenic to the H-2^b background of HHD mice) known in the art (Hatano et al., *J Transl Med.*, 2:40, 2004). The T2 cell line is an HLA-A2⁺, TAP-deficient human T-cell/

Fluorescence Imaging of Tumor Sections.

Tumor tissue samples were prepared and sectioned as previously described (Komita et al., *Cancer Res.*, 68: 8076-8084, 2008). For analysis of T cell subsets, sections were incubated with rabbit anti-mouse NG2 (Millipore, Bedford, Mass.)

along with alexa488-conjugated anti-CD4 or -CD8 β antibodies or matching isotype controls (all from BD Biosciences, San Jose, Calif.) for 1 h. After washing with 0.5% BSA in PBS, sections were stained with donkey anti-rabbit Ig cy5 (Jackson ImmunoResearch, West Grove, Pa.) secondary antibody for one hour at room temperature. For analysis of CD31 vs. NG2, sections were first incubated with rat anti-mouse CD31 (BD Biosciences) and rabbit anti-mouse NG2 (Millipore) antibodies for one hour at room temperature and then washed. Sections were then treated with donkey anti-rat Ig cy3 and donkey anti-rabbit Ig cy5 (both from Jackson ImmunoResearch) antibodies for 1 hr and washed. For the analysis of target antigens in B16 tumor lesions, all sections received dilutions of rat anti-mouse CD31 (BD Biosciences) and guinea pig anti-mouse NG2 (Burg et al. *Cancer Res.*, 59:2869-2874, 1999) antibodies. In addition, each slide received an antibody reactive against a given TASA: rabbit anti-mouse antibody for DLK1 (R&D Systems, Minneapolis, Minn.), EphA2 (Santa Cruz Biotech., San Diego, Calif.), PSMA (Thermo Fisher Scientific, Rockford, Ill.), RGS5 (Sigma-Aldrich), VEGFR1 (Thermo Fisher Scientific) or goat anti-mouse antibody for HBB (Santa Cruz), NRP1 (R&D Systems), NRP2 (R&D Systems), PDGFR β (R&D Systems), VEGFR2 (Abcam, Cambridge, Mass.). Sections were then again washed five times with 0.5% BSA (in PBS), before a one hour incubation with dilutions of a mixture of secondary antibodies: i.) donkey anti-rat cy5 antibody, ii.) donkey anti-guinea pig DyLight 488 antibody, and iii.) either donkey anti-rabbit cy3 antibody or donkey anti-goat cy3 antibody depending on the species of antibody directed against the TASA target (all secondary antibodies were purchased from Jackson ImmunoResearch). After secondary Ab staining, sections were then washed with 3 washes of PBS, coverslipped with gelvatol mounting media (made in-house) and stored at 4° C. until imaging using an Olympus Fluoview 500 Confocal microscope (Olympus America, Center Valley, Pa.).

Synthetic Peptides.

The peptides shown in Table 4 were synthesized by 9-fluorenylmethoxycarbonyl (Fmoc) chemistry. Peptides were >96% pure based on high performance liquid chromatography profile and mass spectrometric analysis.

Generation of HHD Bone Marrow (BM)-Derived DCs and DC.IL12.

DC were generated from BM precursors isolated from the tibias/femurs of mice using in vitro cultures containing 1000 U/ml recombinant murine granulocyte/macrophage colony-stimulating factor (rmGM-CSF) and 1000 U/ml rIL-4 (both from Peprotech, Rocky Hill, N.J.), as previously described (Komita et al., *Cancer Res.*, 68: 8076-8084, 2008). The Ad.mIL-12p70 and Ad. ψ 5 (empty) recombinant adenoviral vectors were produced as reported previously (Komita et al., *Cancer Res.*, 68: 8076-8084, 2008; Tatsumi et al., *Cancer Res.*, 63: 6378-6386, 2003). Five million (day 5 cultured) DCs were infected at an MOI=50 with Ad.mIL-12p70 or the control, empty vector Ad. ψ 5. While control DC produced <62.5 pg IL-12p70/ml/48 h/10⁶ cells, DC.IL12 cells produced 1-10 ng IL-12p70/ml/48 h/10⁶ cells (Komita et al., *Cancer Res.*, 68:8076-8084, 2008; Tatsumi et al., *Cancer Res.*, 63:6378-6386, 2003).

Intratumoral (Lt.) DC.IL12 Therapy.

B16 melanoma cells (1 \times 10⁵) were injected subcutaneously in the right flank of HHD mice and allowed to establish for 7 days. Mice were then randomized into cohorts of 5 animals, with each cohort exhibiting an approximate mean tumor size of 30-50 mm². On days 7 and 14, tumor-bearing mice were untreated or treated with intratumoral injections of 1 \times 10⁶ adenovirus-infected dendritic cells (DC. ψ 5 or DC.IL12) in a

total volume of 50 μ L PBS. Tumor size was then assessed every 3 to 4 days and recorded in mm², determined as the product of orthogonal measurements taken using vernier calipers. In some experiments, as indicated, in vivo antibody depletions (on days 6, 13 and 20 post-tumor injection) of CD4⁺ T cells or CD8⁺ T cells were performed as previously described (13). Data were reported as mean tumor area \pm SD. On day 17-19 post-tumor inoculation, CD8⁺ splenocytes and TIL were MACS-isolated from 3 mice/cohort, with cells pooled and assessed for reactivity against peptide epitopes or cell targets (pericytes, VEC, tumor cells).

Evaluation of Murine CD8⁺ T Cell Responses In Vitro.

To analyze Ag-specific responses, spleens and TIL were harvested (from 2 mice/group) 3-5 days after the second intratumoral injection of control DC or DC.IL12 (i.e. day 17-19 after tumor inoculation). Splenic lymphocytes were restimulated in vitro for 5 days with irradiated (2.5 Gy) naïve peptide-pulsed HHD splenocytes at a stimulator:responder cell ratio of 1:1. Responder CD8⁺ T cells were then isolated using magnetic bead cell sorting (MACS; Miltenyi Biotec) and analyzed for reactivity against unpulsed or peptide-pulsed T2 cells, as indicated. To analyze T cell response to stromal cell targets and tumor cells, untreated HHD mice bearing established day 17-19 B16 tumors were sacrificed and tumors and kidneys removed. Tissues were then minced manually and enzymatically digested as described by Crisan et al. (Crisan et al., *Cell Stem Cell.*, 3:301-313, 2008) using collagenases IA, II, and IV (Sigma-Aldrich) and DNase I (Sigma-Aldrich) for 30 min at 37° C., with gentle shaking. Cells were then being passed through a 70 micron cell strainer (BD-Biosciences), washed with PBS, and single cell suspensions stained with anti-mouse CD31 FITC (BD-Biosciences), anti-mouse CD140b (PDGFR β) PE (eBioscience), and anti-mouse H2-K^b APC (BD-Biosciences). After washing with PBS, cells were sorted into enriched populations containing pericytes (PDGFR β ⁺CD31^{neg}H-2K^b(^{neg})) or VEC (PDGFR β ^{neg}CD31⁺H-2K^b(^{neg})) using a multicolor fluorescence-activated cell sorter (FACSaria, BD-Biosciences). In all cases, cells were >95% pure for the stated phenotype. CD8⁺ T cells (10⁵) were then co-cultured with 10⁴ pericytes or VEC in U-bottom 96-well plates (Sigma-Aldrich). To verify HLA-A2 restricted recognition of target cells by CD8⁺ T cells, 10 μ g of anti-HLA-A2 mAb BB7.2 or control anti-HLA-class II mAb L243 (both from ATCC) were added to replicate co-culture wells. Forty-eight hours after initiating splenic CD8⁺ T cell co-cultures, cell-free supernatants were collected and analyzed for mIFN- γ content using a commercial ELISA (BD-Biosciences) with a lower limit of detection of 31.3 pg/ml. Data were reported as the mean \pm SD of triplicate determinations. Alternatively, freshly-sorted CD8⁺ TIL were co-cultured with pericytes, VEC, T2 cells (+/-peptides) or B16 tumor cells at a T cell-to-target cell ratio of 3:2 for 4-5 h at 37° C. and analyzed for intracellular levels of IFN- γ or cell-surface expression of CD107a/b using specific monoclonal antibodies (APC-labeled anti-mouse CD8 α from eBioscience; PE-labeled rat anti-mouse IFN- γ and FITC-labeled rat anti-mouse CD107a/b from BD Biosciences) and flow cytometry using the manufacturer's suggested protocol and ref. (Mittendorf et al., *Breast Cancer Res Treat.*, 92:85-93, 2005), respectively.

In Vitro Assessment of Human CD8⁺ T Cell Responses Against TASA- or TAA-Derived Peptides.

Peripheral blood mononuclear cells (PBMC) were obtained by venipuncture or leukapheresis from HLA-A2⁺ normal donors or HLA-A2⁺ melanoma patients with written consent under IRB-approved protocols (Table 3). CD8⁺ T cells were then isolated by MACS (Miltenyi Biotec, Auburn,

Calif.) and either not stimulated or stimulated with autologous, TASA peptide-pulsed DC as previously described (Tatsumi et al., *Cancer Res.*, 63:4481-4489, 2003). Normal donor T cells were stimulated with TASA peptide-pulsed DC twice on a weekly schedule, with responder T cells harvested for analysis of their specificity 5 days after the booster stimulation (i.e. day 12 of T cell-DC co-culture). Melanoma patient CD8⁺ T cells were analyzed after a single round of stimulation with TASA peptide-pulsed, autologous DC (i.e. day 5 of T cell-DC co-culture) as indicated. For DC-based stimulations, DC were pulsed with an equimolar (1 μ M each) pool of the TASA peptides (Table 4) for 4 h at 37° C. at 5% CO₂ tension. These antigen-loaded DC were then used to stimulate autologous CD8⁺ T cells at a T cell-to-DC ratio of 10:1 to generate a bulk population of responder T cells. T cells were maintained in IMDM media supplemented with 10% human AB serum, 100 U/ml penicillin, 100 mg/ml streptomycin, 10 mM L-glutamine and MEM non-essential amino acids (all reagents from Invitrogen, except human AB serum that was purchased from Sigma-Aldrich, St. Louis, Mo.). Responder CD8⁺ T cells were analyzed for reactivity against control (HLA-A2*) T2 cells or T2 cells pulsed with individual TASA or TAA peptides (1 μ M for 4 h at 37° C.) at a CD8⁺ T cell-to-T2 cell ratio of 5:1 for 24 h. Harvested cell-free supernatants were consequently assessed for hIFN- γ content using a specific ELISA (BD Biosciences, San Diego, Calif.) with a lower detection limit of 4.7 pg/ml.

Statistical Analysis.

Student's two-sided t-test and one-way ANOVA were used to test for overall differences between groups (StatMate III, ATMS Co., Tokyo, Japan), with a p value <0.05 taken as significant.

Results

Analysis of TASA Expression in the TME.

TASA are expressed by pericytes and/or activated VEC (Komita et al., *Cancer Res.*, 68:8076-8084, 2008; Hatano et al., *J Transl Med.*, 2:40, 2004; Maciag et al., *Cancer Res.*, 68:8066-8075, 2008; Ishizaki et al., *Clin Cancer Res.*, 12:5841-5849, 2006; Wada et al., *Cancer Res.*, 65:4939-4946, 2005; Kaplan et al., *Vaccine*, 24: 6994-7002, 2006; Liu et al., *Cytokine.*, 32:206-212, 2005; Silver et al., *Clin Cancer Res.*, 3:81-85, 1997; Harada et al., *Oncol Rep.*, 12:601-607, 2004; Bondjers et al., *Am J Pathol.*, 162:721-729, 2003; Boss et al., *Clin Cancer Res.*, 13:3347-3355, 2007; Christian et al., *Am J Pathol.*, 172:486-494, 2008). An initial panel of 12 antigens was selected for evaluation in the current studies (Table 4). To show that the chosen TASA were indeed expressed in situ by stromal cells in the TME, immunohistochemistry analyses were performed using specific antibodies on tissue sections isolated from day 14 (HLA-A2^{neg}) B16 melanomas growing progressively in untreated HLA-A2 Tg (HHD) mice. Using immunofluorescence microscopy, co-expression patterns of specific stromal target antigens were determined with NG2⁺ pericytes and/or CD31⁺ VEC within the TME. The resulting images are depicted in FIG. 1A, with a summary of cellular protein expression profiles provided in Table 3. Based on these imaging analyses, the DLK1, HBB, NG2, PDGFR β , RGS5 and VEGFR2 antigens were assigned as predominantly tumor pericyte-associated, and the EphA2 and TEM1 antigens as predominantly tumor VEC-associated. The NRP1, NRP2, PSMA and VEGFR1 antigens appeared to be expressed by multiple cell types including pericytes, VEC and alternate stromal cells and/or tumor cells within the progressive B16 TME. To further corroborate TASA expression by NG2⁺ pericytes, CD31⁺ VEC or H-2K^b tumor cells within the TME, these cell populations were flow-sorted from enzymatically digested B16 tumors resected from untreated

recipient HHD mice. To gauge potential overexpression of TASA in tumor versus normal tissues, pericytes and VEC were also flow-sorted from single cell digests of tumor-uninvolved kidneys harvested from these same animals. RT-PCR analyses were then performed on cDNA isolated from each of these sorted cell populations. Quality control analyses supported the expression of NG2 transcripts only in pericytes, CD31 transcripts only in VEC and gp100 transcripts only in B16 cells (FIG. 1B). These analyses also support: i.) tumor pericyte expression of all TASA transcripts with the exceptions of EphA2 and PSMA; ii.) tumor VEC expression of transcripts for DLK1, EphA2, HBB, PSMA, TEM1, VEGFR1 and VEGFR2; iii.) B16 expression of transcripts for NRP1, PDGFR β , VEGFR1 and VEGFR2; iv.) higher levels of DLK1, EphA2, HBB, NRP1, NRP2, PDGFR β , RGS5, TEM1, VEGFR1 and VEGFR2 transcript expression in tumor- versus normal kidney-derived stromal cells; and v.) comparable or greater levels of NG2, PSMA and CD31 transcript expression in normal kidney- versus tumor-derived stromal cells (FIG. 1B).

TABLE 3

Cells expressing TASA in the B16 TME.*		
TASA	Cells Expressing TASA Protein (IHC)	Cells Expressing TASA mRNA (RT-PCR)
DLK1	P	P (Hi) > VEC (2.1)
EphA2	VEC	VEC (3.3)
HBB	P	P (Hi) > VEC (Hi)
NG2	P	P
NRP1	P, VEC, T/S (Pericyte/VEC interface)	P (2.0), T > VEC
NRP2	P, VEC (Intracellular)	P (1.6)
PDGFR β	P > T/S	P (2.3), T
PSMA	VEC, P (Vesiculated, punctuate)	VEC
RGS5	P > T/S (Cytoplasmic)	P (1.7)
TEM1	T/S, VEC, P	P (1.5), VEC (1.6)
VEGFR1	VEC, P, T/S (Intracellular/Nuclear)	VEC (1.8) > P (2.6), T
VEGFR2	P > VEC, T/S	P (1.6) > VEC (4.5), T

*Progressor B16 tumors (day 14) in untreated HHD mice were surgically-resected, then fixed, sectioned and stained using TASA-specific Abs, as described in FIG. 1A and the Materials and Methods. Based on co-localization of TASA with the NG2 and/or CD31 markers in fluorescence microscopy analyses, a pericyte (P)- and/or VEC- association was assigned with a given marker, respectively. In some cases, TASA were also expressed by NG2^{neg}, CD31^{neg} cells (designated as T/S = tumor/stromal) in the TME, which could reflect either tumor cells or alternate stromal cell populations. RT-PCR analyses were performed on flow-sorted tumor-derived pericytes and VEC and tumor cells as described in FIG. 1B and the Materials and Methods. Numbers in parentheses reflect the fold increase in expression of transcripts in tumor versus normal kidney pericytes or VEC, as indicated, after first normalizing densitometry signals against β -actin in each case. (Hi) indicates the TASA transcript is expressed by tumor pericytes/VEC, but not normal kidney pericytes/VEC.

Selection of TASA Peptides for Immunologic Analyses.

Of the selected TASA, HLA-A2-presented epitopes recognized by CD8⁺ T cells have been previously reported for human EphA2, NG2, PSMA, RGS5, VEGFR1 and VEGFR2 (Table 4). Notably, these defined human epitopes share 100% sequence identity with their murine homologues. To identify novel HLA-A2-presented epitopes in the alternate 6 selected TASA, a prediction algorithm (see, e.g., bimas.cit.nih.gov/molbio/hla_bind/) was applied to each protein, and non-amer (9-mer) and/or decameric (10-mer) peptides were preferentially chosen for synthesis and corollary analyses based on 2 priority criteria: i.) a high algorithm predicted binding score to the HLA-A2.1 class I molecule, and ii.) identity in the human versus murine peptide sequences. This latter restriction was adopted for translational purposes; i.e. to insure that specific therapy-induced T cell responses would need to break operational tolerance in HLA-A2 Tg (HHD) recipient mice in order to provide anti-tumor protection (i.e. as would also need to occur for protection in HLA-A2⁺

patients with solid cancers). After selection, each of the chosen synthetic peptides was shown to be competent (to a varying degree) to bind and stabilize HLA-A2 complexes expressed by T2 cells (FIG. 6), a prerequisite to their ability to be presented to specific, HLA-A2-restricted CD8⁺ T cells.

DC.ψ5)-treated cohort of animals directly recognized HLA-A2⁺ pericytes and VEC flow sorted from single-cell digests of B16 tumors (but not kidneys isolated from these same tumor-bearing animals) or HLA-A2^{neg} B16 tumor cells (FIG. 2B, 2C and FIG. 7). Tc1 recognition of tumor-derived pericytes and

TABLE 4

Summary of in vitro results regarding TASA peptides.*							
TASA	AA Positions	Immunogenic Peptide Sequence	SEQ ID NO:	HLA-A2 Binding Score ^b	Specific CD8 ⁺ T Cell Response ^c		
					HHD Mice Treated With i.t. DC.IL12	HLA-A2+ Normal Donors (of 8)	HLA-A2+ Melanoma Patients (of 10)
DLK1	269-277	RLTPGVHEL	68	49	+	1	4
	310-318	ILGVLTSLV	2	118	+	2	6
	326-334	FLNKCEWV	3	1760	+	2	4
EphA2 ^c	883-891	TLADFDPKV	10	1084	+	2	6
HBB	31-39	RLLVVYPWT	70	227	+	2	6
	105-114	RLLGNVLVCV	72	592	+	1	1
NG2 ^d	770-778	TLSNLSFPV	83	403	—	0	4
	2238-2246	LILPLLFYL	14	1356	—	0	4
NRP1	331-339	GLLRFVTAV	6	2249	+	2	7
	433-441	GMLGMVSGI	75	131	+	2	7
	869-877	VLLGAVCGV	8	1006	+	2	1
NRP2	214-222	DIWDGIPHV	15	56	+	0	4
	328-336	YLQVDLRFL	16	249	+	0	4
	436-444	NMLGMLSGI	17	131	—	0	0
PDGFRβ	890-898	ILLWEIFTL	81	1792	+	2	1
PSMA ^e	441-450	LLQERGVAYI	18	920	+	0	2
RGS5 ^f	5-13	LAALPHSCL	79	1	+	0	5
TEM1	691-700	LLVPTCVFLV	76	1577	+	4	4
VEGFR1 ^g	770-778	TLFWLLLTLL	19	182	+	1	3
VEGFR2 ^h	773-781	VIAMFFWLL	20	270	+	0	0

*CD8⁺ T cell response data is summarized for i.) HHD mice treated with DC.IL-12 gene therapy (as in FIG. 2C) or ii.) HLA-A2⁺ normal human donors and HLA-A2⁺ patients with melanoma as displayed pictorially in FIG. 4. Human (ELISA) responses were designated as + if CD8⁺ T cell reactivity against T2 cells presenting the indicated peptide (IFN-γ) was >30 pg/ml and more than 2 fold higher than reactivity versus T2 cells pulsed with the negative control HIV-nef₁₀₀₋₁₉₈ peptide (p < 0.05).

^bPeptide sequences were submitted to an algorithm predicting binding to HLA-A2, with the deduced scores provided. A higher number reflects the prediction of a more stable HLA-A2-peptide complex.

^c(see Tatsumi et al., *Cancer Res.*, 63: 4481-4489, 2003).

^d(see Maciag et al., *Cancer Res.*, 68: 8066-8075, 2008).

^e(see Harada et al., *Oncol.Rep.*, 12: 601-607, 2004).

^f(see Boss et al., *Clin. Cancer Res.*, 13: 3347-3355, 2007).

^g(see Ishizaki et al., *Clin. Cancer Res.*, 12: 5841-5849, 2006).

^h(see Wada et al., *Cancer Res.*, 65: 4939-4946, 2005).

Delivery of DC.IL12 into HLA-A2^{neg} B16 Tumors Promotes the Cross-Priming of CD8⁺ T Cells Reactive Against Tumor Pericytes, VEC and an Array of TASA-Derived Peptide Epitopes in HHD Mice.

DC.IL12 were prepared and injected directly into subcutaneous (HLA-A2^{neg}) B16 melanomas growing progressively in HLA-A2 Tg HHD mice on days 7 and 14 post-tumor inoculation. On day 19 post-tumor inoculation, the mice were euthanized and CD8⁺ splenic T cells were analyzed for their ability to secrete IFN-γ in response to stimulation with TASA-derived peptides presented by the HLA-A2⁺ T2 cell line.

Intratumoral delivery of DC.IL12 resulted in dramatically reduced tumor growth (FIG. 2A; p<0.05 versus vs. DC.ψ5-treated or untreated controls after day 11). Furthermore, splenic CD8⁺ T cells isolated from the DC.IL12 (but not

VEC was completely blocked in the presence of the anti-HLA-A2 mAb BB7.2 (but not an anti-MHC II mAb L243), supporting the HLA-A2-restricted nature of T cell reactivity. Splenic CD8⁺ T cells from DC.IL12- (but not control DC-) treated animals also responded against an array of TASA-derived peptides when presented by HLA-A2⁺ T2 cells in vitro (FIG. 2C). A non-limiting explanation for ability of these murine (HHD) CD8⁺ T cells to recognize TASA-derived peptides in the context of the human T2 cell line is that these Tc1 effector cells exhibit moderate-to-high avidity for specific epitopes, since the murine CD8 co-receptor interacts inefficiently with the human HLA class I α3 domain (Kuball et al., *Immunity*, 22:117-129, 2005) expressed by T2 cells.

The impact of therapy on the ability of CD8⁺ tumor-infiltrating lymphocytes (TIL) freshly-isolated from day 17

tumors to recognize flow-sorted pericytes and VEC, as well as, TASA peptides presented by T2 cells was assayed. Using both intracellular IFN- γ staining (FIG. 3A) and CD107 translocation (FIG. 3B; i.e. a measure of effector T cell degranulation associated with perforin/granzyme-dependent lysis; (Mittendorf et al., *Breast Cancer Res Treat.*, 92:85-93, 2005) assays, it was observed that 3-12% of CD8⁺ TIL isolated from animals treated with DC:IL12 mediated effector Tc1 responses against tumor (but not kidney)-derived pericytes and VEC. Similar frequencies of CD8⁺ TIL from the DC:IL12-treated cohort of mice recognized TASA peptides presented by T2 cells (FIG. 3A, FIG. 3B). The ability of target cells to elicit effector responses from CD8⁺ TIL isolated from DC:IL12-treated mice was blocked by anti-HLA-A2 (but not anti-class II) mAb and these T cells display only background reactivity against HLA-A2^{neg} B16 tumor cells (FIG. 8). In contrast, the frequency of TASA-specific CD8⁺ TIL isolated from untreated or DC: ψ 5-treated melanoma was lower (versus DC:IL12 treatment) in all functional analyses performed (FIGS. 2C, 3A, 3B, 8).

CD8⁺ T Cells from HLA-A2⁺ Normal Donors or HLA-A2⁺ Melanoma Patients Recognize TASA-Derived Peptides In Vitro.

To assess whether the TASA-derived peptides identified in the HHD tumor model were also capable of being recognized by human CD8⁺ T cells, IVS was performed using T cells isolated from the peripheral blood of HLA-A2⁺ donors or HLA-A2⁺ patients with melanoma. DC were pulsed with peptides derived from a given TASA for 4 h at 37° C., then washed and used as stimulator cells for autologous CD8⁺ T cells. In cases where more than one peptide existed for a given protein, DC were pulsed with an equimolar (10 μ M) mixture of each peptide. Two rounds of IVS using TASA for normal donors and a single-round of IVS using TASA for melanoma patients was applied. HLA-A2⁺ normal donors (FIG. 4; Tables 4, 5A and 5B) and melanoma patients (FIG. 4; Tables 4, 5A and 5B) were each capable of recognizing many of the TASA-derived peptides.

effect occurs via cross-presentation mediated by HLA-A2⁺ APCs emigrating from the TME (Zhang et al., *J Exp Med.*, 204:49-55, 2007).

TABLE 5A

Normal donor and melanoma patient demographics and responsiveness to TASA.*				
Donor	Age	Sex	Stage	Prior Therapy
ND1	51	M	N/A	N/A
ND2	62	F	N/A	N/A
ND3	37	M	N/A	N/A
ND4	28	M	N/A	N/A
ND5	50	F	N/A	N/A
ND6	32	F	N/A	N/A
ND7	26	M	N/A	N/A
ND8	38	F	N/A	N/A
Mel1	62	F	IIA	S
Mel2	69	M	IV	Anti-CTLA4
Mel3	55	F	IIC	C
Mel4	87	F	IIC	MAA- VAC, IL-2
Mel5	65	M	IV	C, R
Mel6	71	M	IV	GM2-KLH
Mel7	56	F	IV	C
Mel8	64	F	IV	C, IFN
Mel9	62	F	IV	C, IFN
Mel10	56	M	IV	C, IFN, IL-2

*Abbreviations used in Table 5A: AD, Active disease; C, Chemotherapy; CTLA-4, Cytotoxic T lymphocyte antigen-4; DC, dendritic cell; F, Female; IFN, Interferon- α , IL-2, Interleukin-2; GM2, Ganglioside M2; KLH, Keyhole limpet hemocyanin; M, Male; NED, No evidence of disease; R, Radiotherapy; S, Surgery; MAA, Melanoma-associated antigen; VAC, Vaccine.

TABLE 5B

Normal donor and melanoma patient demographics and responsiveness to TASA: Specific CD8 ⁺ T cell Production of IFN- γ in Response to TASA.												
Donor	DLK1	EphA2	HBB	NG2	NRP1	NRP2	PFGFR β	PSMA	RGS5	TEM1	VEGFR1	VEGFR2
ND1	+	-	-	-	+	-	-	-	-	+	-	-
ND2	+	-	+	-	+	-	+	-	-	+	-	-
ND3	+	+	-	-	-	-	-	-	-	+	-	-
ND4	-	-	-	-	-	-	+	-	-	-	-	-
ND5	-	+	-	-	+	-	-	-	-	+	+	-
ND6	-	-	-	-	+	-	-	-	-	-	-	-
ND7	-	-	-	-	-	-	-	-	-	-	-	-
ND8	+	-	+	-	-	-	-	-	-	-	-	-
Mel1	+	+	+	-	+	+	-	-	+	+	-	-
Mel2	+	+	+	-	+	+	-	-	+	-	-	-
Mel3	-	+	+	-	+	-	-	-	-	-	-	-
Mel4	+	+	+	+	+	+	-	+	+	+	+	-
Mel5	-	-	-	-	+	+	-	-	-	-	-	-
Mel6	+	+	+	+	+	-	-	+	+	-	+	-
Mel7	-	-	+	-	+	-	-	-	-	+	+	-
Mel8	+	-	-	+	+	-	+	-	+	+	-	-
Mel9	+	+	-	+	-	-	-	-	-	-	-	-
Mel10	-	-	-	-	-	-	-	-	-	-	-	-

As shown in FIG. 5, in the HHD recipient mouse model system, protective HLA-A2-restricted Tc1 cells failed to recognize HLA-A2^{neg} B16 tumor cells, even though CD8⁺ T cells appeared to be cross-primed against HLA-A2-presented B16 melanoma-associated antigens such as MART-1 and gp100. A non-limiting explanation for this result is that the

Human responses were designated as + if T cell reactivity against T2 cells presenting the indicated peptide (IFN- γ ELISA) was >30 pg/ml and more than 2 fold higher than reactivity versus T2 cells pulsed with the negative control HIV-nef₁₉₀₋₁₉₈ peptide (with p<0.05 versus T2+HIV-nef₁₉₀₋₁₉₈).

Without being bound by theory, this data suggests the translational utility of TASA peptides in the context of active vaccination protocols and/or clinical trials implementing immunotherapeutic/anti-angiogenic approaches (including IL-12p70 gene therapy, tyrosine kinase inhibitors (TKI) or VEGFR antagonists) for the treatment of solid cancers, such as melanoma.

Example 2

Vaccines Targeting Tumor Blood Vessel Antigens Promote CD8⁺ T Cell-Dependent Tumor Eradication or Dormancy in HLA-A2 Transgenic Mice

This example illustrates that therapeutic vaccination of HHD mice with TBVA-peptides results in CD8⁺ T cell-dependent regression of colon carcinoma and melanoma and long-term protection against disease relapse.

Materials and Methods

Mice.

HHD mice are D^b×β₂-microglobulin (β₂M) null, transgenic for the modified HLA-A*0201-hβ₂-microglobulin single chain (HHD gene; Firat et al., 1999, *Eur. J. Immunol.* 29: 3112-3121) and exhibit CD8⁺ T cell responses that recapitulate those observed in HLA-A2⁺ human donors (28-30). C57BL/6 wild-type mice were purchased from The Jackson Laboratory (Bar Harbor, Me.). Female 6-8 week old mice were used in all experiments and were handled in accordance with an Institutional Animal Care and Use Committee (IACUC)-approved protocol.

Cell Lines.

MC38, a methylcholanthrene-induced (HLA-A2^{neg}) murine colon carcinoma cell line and B16 an HLA-A2^{neg} melanoma cell line (syngenic to the H-2^b background of HHD mice) have been described previously (Yamaguchi et al., 2007, *Cancer* 110: 1469-1477, Hatano et al., 2004, *J. Transl. Med.* 2: 40). The T2 cell line is a TAP-deficient T-cell/B-cell hybridoma that constitutively expresses HLA-A2 (Stuber et al., 1994, *Eur. J. Immunol.* 24: 765-768). All cell lines were free of *Mycoplasma* contamination.

Peptides.

All peptides were synthesized using 9-fluorenylmethoxycarbonyl (Fmoc) chemistry. Peptides were >96% pure based on high performance liquid chromatography profile and mass spectrometric analysis.

Production of Murine Bone Marrow (BM)-Derived DCs and DC:IL12.

DC were generated from BM precursors isolated from the tibias/femurs of HHD mice, as previously described (28). The Ad mIL-12p70 and Ad.ψ5 (empty) recombinant adenoviral vectors were produced as reported previously (34). Five million (day 5 cultured) DCs were infected at MOI=50 with Ad mIL-12p70 or the control, empty vector Ad.ψ5. While control DC produced <62.5 pg IL-12p70/ml/48 h/10⁶ cells, DC:IL12 cells produced 1-10 ng IL-12p70/ml/48 h/10⁶ cells (Komita et al., *Cancer Res.*, 68:8076-8084, 2008).

Vaccine Experiments.

For prophylactic experiments, HHD mice were immunized subcutaneously on the right flank with 100 μl PBS or PBS containing 10⁶ syngenic DC:IL12 cells that had been untreated or pre-pulsed for 4 h at 37° C. with 10 μM synthetic peptide(s). Immunizations occurred on days-14 and -7, with mice subsequently receiving injections of MC38 (2×10⁶) tumor cells in the left flank on d0. In all cases, treatment groups contained 5 mice per cohort. For analysis of tumor cellular composition in repeat experiments, MC38 tumors were isolated by surgical resection 10 days after tumor inocu-

lation and prepared for fluorescence imaging, as described below. For therapeutic experiments, MC38 (2×10⁶) or B16 melanoma cells (1×10⁵) were injected subcutaneously in the right flank and allowed to establish/progress for 7 days, at which time, the mice were randomized into cohorts of 5 mice each, with each group exhibiting an approximate mean tumor size of 50-75 mm². Mice were then untreated or treated with control, syngenic DC:IL12 or DC:IL12 (10⁶ cells injected subcutaneously in the left flank on days 7 and 14) pulsed with synthetic TBVA peptides. In some assays, as indicated, in vivo antibody depletions (on days 6, 13 and 20 post-tumor inoculation to assess early involvement or on days 60 and 67 or 180 and 187 to assess late involvement) of protective CD4⁺ T cells or CD8⁺ T cells were performed and monitored as previously described (Zhao et al., *Mol Ther.*, 19:805-814, 2011). In all cases, tumor size (area) was monitored every 3-4 days and is reported as mean±SD in mm².

Evaluation of Specific CD8⁺ T Cell Responses in HHD Mice.

MACS (Miltenyi Biotec) CD8⁺ splenocytes were harvested (from 3 mice/group) 7 days after the second round of DC-based vaccination (i.e. day 21 after tumor inoculation) and analyzed for reactivity against unpulsed T2 cells, TBVA peptide-pulsed T2 cells, or day 19 (flow-sorted) B16-derived PDGFRβ⁺CD31^{neg}H-2K^{b(neg)} pericytes or PDGFRβ^{neg}CD31⁺H-2K^{b(neg)} VEC isolated as previously described (Zhao et al., *Mol Ther.*, 19:805-814, 2011). Where indicated, 10 μg of anti-HLA-A2 mAb BB7.2 or control anti-class II mAb L243 (both from ATCC, Manassas, Va.) were added to replicate co-culture wells. After 48 h, supernatants were analyzed for mIFN-γ content by specific ELISA (BD-Biosciences; lower detection limit=31.3 pg/ml). Data are reported as the mean±SD of triplicate determinations.

RT-PCR.

Reverse transcriptase-PCR (RT-PCR) was performed using primer pairs as described in Example 1.

Fluorescence Imaging of Tumor Sections.

Tumor tissue samples were prepared and 6 micron sections prepared as previously reported (Komita et al., *Cancer Res.*, 68:8076-8084, 2008). The following Abs were used: (for T cell analyses), rabbit anti-mouse NG2 (Millipore, Bedford, Mass.) and alexa488-conjugated anti-CD4 or -CD8β antibodies or matching isotype controls (all from BD-Biosciences); (for vascular analyses), rat anti-mouse CD31 (BD-Biosciences) and rabbit anti-mouse NG2 (Millipore) Abs; (for TBVA), rat anti-mouse CD31 (BD-Biosciences) and guinea pig anti-mouse NG2 Abs, along with anti-TBVA as described in Example 1. Imaging was performed using an Olympus Fluoview 500 Confocal microscope (Olympus America, Center Valley, Pa.).

Cutaneous Wound Healing Assays.

Wound healing analyses were performed in HHD mice as described by Maciag et al. (Maciag et al., *Cancer Res.*, 68:8066-8075, 2008).

Statistical Analysis.

Two-tailed Student's t-test or two-way ANOVA were used to test overall differences between groups (StatMate III, ATMS Co., Tokyo, Japan), with p-values <0.05 considered significant.

Results

Vaccines Incorporating Peptide Epitopes Derived from TBVA are Immunogenic and Protect HHD Mice Against HLA-A2^{neg} MC38 Tumor Challenge.

To assess the immunogenicity of TBVA-derived peptides, female HLA-A2 Tg (HHD; lacking murine H-2^b class I molecules) mice were vaccinated twice on a weekly schedule with 10⁶ peptide-pulsed, (HHD) DC:IL12 cells. One week

after the booster immunization, CD8⁺ splenocytes were isolated and analyzed for their ability to secrete IFN- γ in response to peptide-pulsed HLA-A2⁺ T2 cells in vitro. As shown in FIG. 9A, the majority (17/20; $p < 0.05$ versus T cells stimulated with DC only) of TBVA-derived peptides analyzed primed Tc1 responses in vivo that could be detected in vitro.

The DLK1, EphA2, HBB, NG2, NRP1, NRP2, PDGFR β , PSMA, RGS5, TEM1, VEGFR1 and VEGFR2 antigens were expressed in situ by blood vessel cells in the MC38 colon carcinoma TME (FIG. 14). Protection of HHD mice against a challenge with HLA-A2^{neg} MC38 tumor cells injected subcutaneously on day zero was assayed with immunization with TBVA-derived peptides on days -14 and -7. As depicted in FIG. 9B, vaccines incorporating peptides from the TBVA DLK1, EphA2, HBB, NRP1, PDGFR β , RGS5 or TEM1 were effective in preventing HLA-A2^{neg} MC38 tumor establishment or they resulted in the regression of tumors (after a transient period of establishment) in HHD mice. In contrast, vaccines based the TBVA NG2, NRP2, PSMA, VEGFR1 or VEGFR2 yielded minimal protection (FIG. 9B). Based on the data provided in FIG. 9, vaccine immunogenicity and efficacy were not always correlated with one another in the MC38 prophylaxis model (FIG. 16), a finding in accordance with reports for peptide-based vaccines in human clinical trials (Jandus et al., *Pigment Cell Melanoma Res.*, 22:711-723, 2009; Vujanovic and Butterfield, *J. Cell. Biochem.*, 102:301-310, 2007; Yu and Restifo, *J. Clin. Invest.*, 110:289-294, 2001).

Protective Vaccines Incorporating TBVA Peptides Promote Enhanced Infiltration of the TME by CD8⁺ T Cells in Association with an Inhibition of Tumor Vascularity.

MC38 tumor lesions from all cohorts of animals with evidence of disease on day 14 (post-tumor inoculation) were isolated and immunofluorescence microscopy on tumor sections was performed. Although control (untreated or vaccinated with DC.II.12/no peptide) mice contained few CD8⁺ T cells in the TME, the majority of the peptide vaccinated cohorts exhibited a variable, but significantly elevated number of CD8⁺ TILs (FIG. 10A, FIG. 10B). In marked contrast, CD4⁺ T cell infiltration in the TME was sparse and the data were indistinguishable when comparing control vs. vaccinated mice (FIG. 17). An analysis of vascular structures in these tumors revealed that mice pre-vaccinated with peptides derived from the TBVA EphA2, RGS5 or TEM1 had the greatest degree of suppression in CD31⁺ vessel counts in the MC38 TME, with somewhat less pronounced effects also noted for groups vaccinated against HBB or VEGFR2 (FIG. 10C, 10D; $p < 0.05$ vs. untreated mice or mice vaccinated with DC.II.12/no peptide). Correlative analyses indicated an association between the anti-tumor efficacy of vaccines and their ability to promote CD8⁺ T cell infiltration and reduced vascularity in the TME (FIG. 16).

Therapeutic Vaccines Incorporating TBVA-Derived Peptide Epitopes are Effective Against Established HLA-A2^{neg} MC38 Colon Carcinomas and HLA-A2^{neg} B16 Melanomas in HHD Mice.

Given the robust anti-tumor activity noted for vaccines based on a subset of TBVA in the prophylactic model, the efficacy of these vaccines as immunotherapies in mice bearing established day 7 subcutaneous MC38 or B16 tumors was assayed. In the MC38 model, HHD mice were treated with DC.II.12 cells pulsed with (an equimolar mixture of) peptides derived from TBVA shown most capable of regulating tumor growth under prophylactic conditions (FIG. 9B) and exhibiting the highest degree of immunogenicity based on data provided in FIG. 9A (i.e. DLK1₃₂₆₋₃₃₄, EphA2₈₈₃₋₈₉₁, HBB₃₁₋₃₉, NRP1₈₆₉₋₈₇₇, PDGFR β ₈₉₀₋₈₉₈, RGS5₅₋₁₃ and TEM1₆₉₁₋₇₀₀). As shown in FIG. 11A, the combination peptide vaccine effectively promoted the regression of established MC38 tumors. Furthermore, based on Ab-depletion analyses, therapeutic benefit was largely due to the action of CD8⁺, but not CD4⁺, T cells (FIG. 11A).

Therapeutic vaccines applied to mice bearing B16 melanomas were also effective in suppressing tumor growth if: i) the vaccine-incorporated peptides derived from the stromal antigens DLK1, EphA2, HBB, NRP1, RGS5 (and to a lesser extent TEM1) and ii) recipient mice were competent to respond to these peptides in an HLA-A2-restricted manner (FIG. 11B). Hence, none of the vaccines evaluated perturbed B16 tumor growth in syngenic B6 mice, which fail to express the relevant HLA-A2 class I restriction element required for CD8⁺ T cell recognition of the immunizing peptides.

HHD Mice Cured of B16 Tumors by TBVA Peptide-Based Therapeutic Vaccines Exhibit Extended Survival and Durable Tc1 Responses Against Tumor-Associated Pericytes and/or VEC, and Spreading in Anti-TBVA CD8⁺ T Cell Repertoire.

Mice treated as in FIG. 11B were followed through 60 days post-tumor inoculation and observed significant survival benefits if the animals had been treated with vaccines containing peptides derived from the TBVA DLK-1, EphA2, HBB, NRP1, RGS5 or TEM1 (FIG. 11C, Table 6). To analyze the status and specificity of Tc1 cells, HHD mice rendered free of B16 melanoma after therapeutic vaccination with DLK or RGS5 peptide-based vaccines were sacrificed 60 days after tumor inoculation. Fresh MACS-isolated spleen CD8⁺ T cells were then analyzed for reactivity against HLA-A2⁺PDGFR β ^{neg}CD31^{neg} pericytes, HLA-A2⁺PDGFR β ^{neg}CD31⁺ VEC or HLA-A2^{neg} tumor cells flow-sorted from day 19 B16 tumors growing progressively in untreated HHD mice. As shown in FIG. 12, splenic Tc1 cells isolated from mice cured after vaccination with DLK1 peptides recognized tumor-associated pericytes and VEC in an MHC class I-restricted manner. They failed to recognize pericytes or VEC isolated from the tumor-uninvolved kidneys of these same donor animals. These Type-1 CD8⁺ T cells strongly recognized the DLK1 peptides used in the protective vaccine formulation, but also (to a variable degree), a number of additional TBVA-derived peptides that were not included in the therapeutic vaccine. Similarly, B16-bearing HHD mice cured using a vaccine based on the RGS5₅₋₁₃ peptide, demonstrated clear Tc1 recognition of tumor (but not tumor-uninvolved kidney) pericytes, as well as, statistically-significant response against HLA-A2⁺ T2 cells pulsed with peptides derived from the TBVA DLK1, EphA2, NG2, NRP1, PSMA, RGS5 or TEM1 (FIG. 12).

TABLE 6

In vivo immunogenicity and anti-tumor efficacy of TBVA-based vaccines in HHD models.*							
TASA	AA Positions	Peptide Sequence	SEQ ID NO	Tc1 Response to Peptide Vaccine (HHD) ^a	Anti-tumor efficacy in MC38 protection model ^b	Anti-tumor efficacy in B16 therapy model (survival: pvalue) ^c	
DLK1	269-277	RLTPGVHEL	68	+	+	.0013	
	310-318	ILGVLTSLV	2	+			
	326-334	FLNKCETWV	3	+			
EphA2	883-891	TLADFDPRV	10	+	+	.0012	
HBB	31-39	RLLVVYPWT	70	+	+	.0012	
	105-114	RLLGNVLVCV	72	+			
NG2	770-778	TLNLSFPV	83	-	+	NS	
	2238-2246	LILPLLFPYL	14	+			
NRP1	331-339	GLLRFVTAV	6	+	+	.0013	
	433-441	GMLGMVSGL	75	+			
	869-877	VLLGAVCGV	8	+			
NRP2	214-222	DIWDGIPHV	15	+	-	NT	
	328-336	YLQVDLRFL	16	-			
	436-444	NMLGMLSGL	17	-			
PDGFRβ	890-898	ILLWEIFTL	81	+	+	NS	
PSMA	441-450	LLQERGVAYI	18	+	-	NT	
RGS5	5-13	LAALPHSCL	79	+	+	.0012	
TEM1	691-700	LLVPTCVFLV	76	+	+	.0102	
VEGFR1	770-778	TLFWLLLTLL	19	+	+/-	NS	
VEGFR2	773-781	VIAMFFWLL	20	+	+/-	NS	

*Data are summarized from FIG. 9 and FIG. 11.

^a+, p < 0.05 versus DC only.

^bVaccines consisted of DC:IL12 pulsed with a pool of 1 or more peptides derived from the indicated TBVA. +/-, p < 0.05 versus DC only for 2 consecutive time points; +, p < 0.05 versus DC only for >2 consecutive time points; - not significant at any time point analyzed.

^cp-value versus mice treated with DC only vaccine (from FIG. 11C). NS, not significant; NT, not tested.

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HHD Mice Cured of B16 Tumors by TBVA Peptide-Based Therapeutic Vaccines Either Exhibit True “Molecular Cures” or a State of CD8⁺ T Cell-Mediated Tumor Dormancy.

Effectively-treated HHD mice with no evidence of (macroscopic) disease were depleted of CD8⁺ or CD4⁺ T cells on days 60 and 67, or 180 and 187 by injection of specific antibodies in vivo. As shown in FIG. 13, depletion of CD8⁺ T cells, but not CD4⁺ T cells, resulted in the re-establishment of melanoma growth at sites of the primary tumor placement in 7/9 (i.e. 78% for depletions on days 60/67) and 3/8 (i.e. 38% for depletions on days 180/187) cases, respectively. Interestingly, 2/9 (22%) mice in the day 60/67 CD8⁺ T cell-depleted group exhibited transient tumor expansion and then “spontaneous” regression over a period of weeks-to-months (FIG. 13); a non-limiting explanation for this finding is that TBVA/tumor-specific CD8⁺ T effector cells recovered in these animals. Additionally, at the time of primary disease recurrence in CD8⁺ T cell-depleted animals, melanomas did not present in distal cutaneous sites and that metastases were not detected in the lung, liver or brain based on a histopathology examination of resected tissues.

To show that that prior vaccination against TASA does not inhibit wound-healing in HHD mice, female HHD mice (5 animals/cohort) were vaccinated in the right flank on d-14 and d-7 with saline, 106 DC:IL12 alone or 106 DC:IL12 pulsed with peptides derived from the indicated TASA. In cases

where more than one peptide is identified for a given TASA, an equimolar pool of the indicated peptides (each 10 μM) was pulsed onto DC:IL12 and used for vaccination in the relevant cohort. On d0, mice were anesthetized, with skin on the upper back shaved and sterilized topically, before placement of two 3-mm diameter wounds using a sterilized punch biopsy instrument. Wounds were not treated consequently and no infections were observed in any animals. The time to closure for the 10 wounds/cohort (2 sites/animal×5 mice/group) was assessed daily and is reported as the mean number of days±SD for complete wound closure (FIG. 18).

To determine expression of selected TASA in tissue, RT-PCR analysis of “stromal” antigen expression by pericytes, VEC and tumor cells in MC38 tumor-bearing mice was examined (FIG. 15). MC38 colon carcinoma cell lines, as well as, flow-sorted tumor- and tumor-uninvolved kidney-associated pericytes and VEC (isolated from HHD mice bearing untreated day 14 tumors) were analyzed for expression of the indicated mRNAs using RT-PCR. As shown in FIG. 15, several of the selected TASA were expressed in the examined tissue.

Thus, a subset of TBVA-derived peptides elicit protective/therapeutic immunity against HLA-A2^{neg} (MC38 or B16) transplantable tumors in HHD mice due to the apparent CD8⁺ T cell targeting of HLA-A2⁺ pericytes or VEC in the TME. Without being bound by theory, because similar peptide-

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based vaccines applied to CD8-depleted HHD mice or HLA-A2^{neg} recipient (C57BL/6) mice failed to yield treatment benefit, indicating involvement of CD8⁺ T cells and the need for these effector cells to target HLA-A2⁺ stromal cells in vivo. Additionally, many responders in the therapeutic vaccine models retained occult disease, since CD8⁺, but not CD4⁺, T cell depletion of such animals resulted in the rapid recurrence of tumors selectively at the site of the original primary lesion in many cases. While in most instances, recurrent tumors grew quickly and proved lethal, in some cases (i.e. 2/10), tumors grew slowly and subsequently underwent spontaneous regression presumably after the Ab-depleted CD8⁺ T cell repertoire had recovered. Without being bound by theory, these data indicate that TBVA peptide-based vaccines can promote either complete eradication of tumors or the establishment of a state of (occult) tumor dormancy over extended periods of time which is regulated by vaccine-instigated CD8⁺ T cells.

Example 3

Therapeutic Vaccination Against Tumor Pericyte-Associated Antigen DLK1

This example provides evidence that the NOTCH antagonist delta-like kinase-1 (DLK1) peptides can be used therapeutically, such as, but not limited to, in treatments for renal cell carcinoma.

Renal cell carcinoma is highly-vascularized and refractory to conventional chemo-/radio-therapy (Motzer and Bukowski, *J Clin Oncol.* 2006; 24:5601-5608). Current first-line therapeutic agents for RCC patients include anti-angiogenic drugs (such as tyrosine kinase inhibitors (TKI) or anti-VEGF antibodies) have yielded high rates of objective clinical response (Escudier et al., *J Clin Oncol.* 2009; 27:4068-4075; Najjar and Rini, *Ther Adv Med Oncol.* 2012; 4:183-194). However, responder patients typically relapse quickly based on the evolution of treatment-refractory disease (Helfrich et al., *J Exp Med.* 2010; 207:491-503). Given such limitations in durable clinical benefits associated with existing treatment options, there remains a great need to develop alternative and/or improved therapies for patients with RCC. In this regard, RCC is considered an immunogenic cancer as patients may exhibit immune-associated spontaneous or therapeutic tumor regression (Finke et al., *Ann NY Acad Sci.* 1988; 532:387-394; Muul et al., *J Immunol.* 1987; 138:989-995; Lokich, *Am J Clin Oncol.* 1997; 20:416-418). Hence, novel therapies capable of improving the magnitude and recruitment of protective immunity into the TME could expand and prolong clinical benefits, and their development remains a mandate.

High-dose cytokine therapy promotes durable complete responses in a minority of treated RCC patients, however, off-target toxicities have limited general use of this approach (Biswas and Eisen, *Nat Rev Clin Oncol.* 2009; 6:478-487), and more specific/focused immunotherapy approaches are warranted. Vaccines targeting cancer cell-associated antigens are safe and immunogenic in the clinical setting, but they have limited curative value (Vujanovic and Butterfield, *J Cell Biochem.* 2007; 102:301-310). While many factors could limit the effectiveness of current cancer vaccines, major obstacles to success include poor delivery and/or functional stability of vaccine-induced tumor infiltrating lymphocytes (TIL) and phenotypic heterogeneity of tumor cell populations permitting immune evasion in vivo (Ahmed et al., *Curr Cancer Drug Targets.* 2008; 8:447-453; Zhao et al., *J Immunol.* 2012; 188:1782-1788). To circumvent such limitations to treatment

success, vaccines promoting specific Tc1 recognition of tumor vascular cell (i.e. pericytes, VEC) populations can be used (see, for example, Komita et al., 2008, *Cancer Res.* 2008; 68:8076-8084).

As disclosed below, pericytes isolated from RCC, but not normal kidney tissue, express the DLK1 antigen in vivo. Using immunofluorescence microscopy and real-time PCR the NOTCH antagonist delta-like kinase-1 (DLK1) was identified as an antigen differentially expressed by blood vessel pericytes in highly-vascularized renal cell carcinoma (RCC) tumors, but not in normal kidney tissue. DLK1 peptide- and gene-based vaccines applied to mice bearing established RCC tumors provided therapeutic benefits in association with tumor blood vessel normalization (based on decreased vascular permeability and intratumoral hypoxia) and the activation and recruitment of CD8⁺ T cells into the tumor microenvironment (TME). Post DLK1-based vaccination, the TME was characterized by increased expression of VCAM1⁺ CD31⁺ vascular endothelial cells and the CXCL10 (IP-10) chemokine associated with superior recruitment of Type-1 (IFN- γ producing) proinflammatory T effector cells and a dramatic reduction in Jarid1B⁺, CD133⁺ and CD44⁺ stem cell populations.

DLK1 peptide- or gene-based vaccines are both immunogenic and therapeutic in the RENCA model of RCC. Effectively treated RCC tumors displayed vascular normalization based on reduced vascular leak and tissue hypoxia, and were highly-infiltrated by CD8⁺ TIL in the perivascular space. Residual pericytes in the TME were tightly-approximated to CD31⁺ VEC and were deficient in expression of DLK1, supportive of vaccine-induced immunoselection of mature mural cell populations in vivo. The results support that vaccines targeting tumor-associated vascular antigens can be used for RCC therapy, and for the treatment of other vascularized solid cancers. Vaccines promoting immune targeting of tumor-associated vascular cells are a therapeutic modality permitting durable normalization of blood vessels in solid cancers, including RCC

Material and Methods

Mice.

Female 6-8 week old BALB/c mice were purchased from The Jackson Laboratory (Bar Harbor, Me.) and maintained in a pathogen-free animal facility.

Tumor Cells.

The mouse renal cell carcinoma cell line RENCA was purchased from the American Type Culture Collection (ATCC, Manassas, Va.) and cultured in complete media as previously reported (Komita et al. *Cancer Res.* 2008; 68:8076-8084). The cell line was negative for known mouse pathogens, including mycoplasma.

Stromal Cell Isolation.

Human RCC tumor and adjacent (patient-matched) normal kidney specimens were analyzed. Murine RCC tumors and tumor uninvolved kidneys were harvested surgically after euthanasia, 21 days after s.c. injection of 10⁶ RENCA cells into syngenic BALB/c recipient animals. Human and murine tissues were then minced manually, enzymatically digested, and pericytes and VEC isolated by flow sorting, as previously described (Crisan et al., *Cell Stem Cell.* 2008; 3:301-313). Murine cells were labeled with anti-mouse CD34-FITC (eBioscience, San Diego, Calif.), anti-mouse CD146-PE (BD-Biosciences, San Diego, Calif.), and anti-mouse CD45-APC (BD-Biosciences) prior to sorting into pericyte (CD146⁺CD34^{neg}CD45^{neg}) and VEC (CD146⁺CD34⁺CD45^{neg}) populations using a multi-color fluorescence-activated cell sorter (FACSARIA; BD Biosciences). In all cases, cells were >95% pure for the stated phenotype.

Real-Time PCR.

Messenger RNA was isolated from pericytes and VEC using the RNeasy® Plus Micro kit (Qiagen, Valencia, Calif.) according to manufacturer's instructions. cDNA was then generated using High Capacity RNA-to-cDNA kit (Applied Biosystems, Carlsbad, Calif.) according to manufacturer's instructions. Real-time PCR was performed using Fast SYBR® Green Master Mix (Applied Biosystems) with primer pairs for human or mouse HPRT1 (Qiagen), human DLK1 (Applied Biosystems) or mouse DLK1 (forward primer: TGTGACCCCCAGTATGGATT, SEQ ID NO: 63, reverse primer: CCAGGGGCGAGTTACACACTT, SEQ ID NO: 64). Reactions were performed in duplicate in a 96-well reaction plate on a StepOnePlus real-time PCR thermocycler (Applied Biosystems). Cycling conditions were 95° C. for 20 min., then 35 cycles of 95° C. for 3 min. and 60° C. for 30 min.

In Vitro Generation of Bone Marrow-Derived Dendritic Cells (DC) and DC:IL12.

DC were generated in 5-day rIL-4+rGM-CSF-supplemented cultures from bone marrow precursors isolated from the tibias/femurs of BALB/c mice infected with recombinant adenovirus encoding mouse IL-12p70 (yielding DC:IL12), as previously described (Zhao et al., *Mol Ther.* 2012; 19:805-814).

Synthetic Peptides.

The H-2^d class I-presented DLK1₁₅₈₋₁₆₆ (CPPGFSGNF; presented by H-2L^d), DLK1₁₆₁₋₁₆₉ (GFSGNFCEI; presented by H-2K^d), DLK1₂₅₆₋₂₇₀ (TILGVLTSLVVL; containing overlapping DLK1₂₅₉₋₂₆₇ and DLK1₂₆₂₋₂₇₀ sequences presented by H-2K^d) peptide were synthesized as previously described (Zhao et al., *J Immunol.* 2012; 188:1782-1788).

Recombinant Lentiviral Vector Production.

Genes encoding mDLK1 and the reverse sequence of mRGSS (as a negative control) were cloned into the pLenti/V5 D-TOPO vector downstream of the CMV promoter using the Lentiviral Directional TOPO® Expression Kit (Invitrogen, Grand Island, N.Y.). To determine insert presence in the plasmid, expression of the V5 tag was detected by immunofluorescence using an anti-V5 FITC antibody (Invitrogen) and by Western blot using an anti-V5 HRP antibody (Invitrogen). In the initial production of the lentiviruses, 293FT cells (Invitrogen) were transfected with plasmid DNA pLenti-DLK1 (or pLenti-NEG) using VIRAPOWERTM Packaging Mix (Invitrogen) combined with Lipofectamine 2000 (Invitrogen) according to the manufacturer's instructions. After 48 hours, lentivirus was collected and concentrated using a Fast-Trap Virus Purification and Concentration kit (Millipore). Lentiviral (lvDLK1 and lvNEG) titers, reported in transduction units (TU), were determined by quantitating blasticidin (Invitrogen)-resistance in HT-1080 cells according to the manufacturer's instructions. Expanded lentiviral production was performed by the University of Pittsburgh Cancer Institute Lentiviral Vector Core Facility. Lentivirus quality was assessed by infecting HT-1080 cells for 24 h and monitoring cells for coordinate V5 protein expression (Western blot) and cell-surface expression of DLK1 (flow cytometry using an anti-DLK1-PE antibody; Adipogen, San Diego, Calif.).

Animal Therapy Experiments.

BALB/c mice received s.c. injection of 10⁶ RENCA tumor cells (right flank) on day 0. Six days later, the animals were randomized into cohorts of 5 mice with comparable mean tumor sizes. On days 7 and 14 after tumor implantation, mice were treated with 100 µl s.c. injections (left flank) of PBS, 10⁶ DC:IL12 or 10⁶ DC:IL12 that had been pre-pulsed for 2 h at 37° C. with an equimolar (10 µM) mixture of the DLK1₁₅₈₋₁₆₆, DLK1₁₆₁₋₁₆₉ and DLK1₂₅₉₋₂₇₀ peptides. For lentivirus vaccination experiments, randomized BALB/c

mice bearing established (day 10; right flank) s.c. RENCA tumors received a single left flank intradermal injection of lvDLK1 or negative control lvNEG at a dose of 40 TU or 200 TU in a total volume of 50 µl PBS. For all animal experiments, tumor size was assessed every 3 to 4 days and recorded in mm², as determined by the product of orthogonal measurements taken using vernier calipers. Data are reported as mean tumor area ±SD.

Evaluation of Specific CD8⁺ T Cell Responses In Vitro.

Spleens were harvested from 3 mice per group 7 days after the second DC injection. Splenocytes were then stimulated in vitro for 5 days with syngenic DC pulsed with an equimolar (10 µM) mix of the 3 DLK1 peptides applied in the vaccine. Responder CD8⁺ T cells were then isolated using magnetic bead cell sorting (Miltenyi Biotec) and co-cultured with DC pulsed with individual DLK1 peptides for 72 h, 37° C. and 5% CO₂, at which time cell-free supernatants were analyzed for IFN-γ content using a cytokine-specific ELISA (BD-Biosciences).

Fluorescent Imaging of Tumors.

Tumor tissue samples were prepared and sectioned as previously reported (Komita et al., *Cancer Res.* 2008; 68:8076-8084). Six-micron tissue sections were analyzed for expression of CD31 (BD-Biosciences), VCAM1 (R & D Systems, Minneapolis, Minn.), CXCL10 (R & D Systems), NG2 (Millipore, Billerica, Mass.), DLK1 (Santa Cruz), RGS5, Jarid1b (all from Abcam; Cambridge, Mass.), CD133 (BD-Biosciences), CD44 (Abcam) by immunofluorescence microscopy. For analysis of cellular apoptosis, tissue sections were labeled using TUNEL kit (Roche; Indianapolis, Ind.) as per manufacturer's instructions, followed by incubation with secondary anti-streptavidin Cy3 antibody (Jackson ImmunoResearch, West Grove, Pa.). Some sections were analyzed by confocal microscopy to generate 30 µm 3-dimensional reconstructions of images. For the vascular permeability imaging, animals received retro-orbital intravenous injections of FITC-labeled tomato lectin (Sigma) and red 20 nm FLUOSPHERES® (Invitrogen), followed by cardiac perfusion of PBS and 4% paraformaldehyde. Tumors were then immediately resected and imaged by confocal microscopy to generate 17 µm 3-dimensional reconstructions.

Hemoglobin Quantitation.

The amount of hemoglobin contained in tissues was quantitated using the Drabkin method (Klungsoyr et al., *Scand J Clin Lab Invest.* 1954; 6:270-276). Hemoglobin content is reported as µg Hb per mg wet weight of tissue.

Measurement of Tumor Hypoxia Using Pimonidazole.

BALB/c mice bearing established (treated or untreated) day 21 s.c. RENCA tumors were injected intraperitoneally (i.p.) with 60 mg/kg pimonidazole hydrochloride (HYPDX-YPROBE™; HPI Inc., Burlington, Mass.) 30 min prior to euthanasia and tumor harvest and 6 µm tissue sections prepared and analyzed by immunohistochemistry as previously reported (Komita et al., *Cancer Res.* 2008; 68:8076-8084).

Statistical Analysis.

Comparisons between groups were performed using a two-tailed Student's t test or one-way Analysis of Variance (ANOVA) with Tukey post-hoc analysis, as indicated. All data were analyzed using SigmaStat software, version 3.5 (Systat Software, Chicago, Ill.). Differences between groups with a p-value <0.05 were considered significant.

Results

RCC-Associated Pericytes Differentially Express the DLK1 Antigen.

In the previous analysis of the therapeutic vaccines incorporating peptides derived from each of twelve individual tumor blood vessel-associated antigens, it was noted that

vaccines targeting delta-like kinase-1 (DLK1) were most effective in HLA-A2 transgenic recipient mice. To apply DLK1 peptide and gene-based vaccines to the only available transplantable murine model of RCC, RENCA, the pattern of DLK1 expression by cells within the TME was first investigated. RENCA tumors and tumor-uninvolved normal kidneys were removed from syngenic BALB/c mice and processed into single cell suspensions. Pericytes and VEC were then isolated via flow sorting (FIG. 19A) and their extracted mRNA (along with mRNA from the cultured RENCA cell line) analyzed by real-time PCR for DLK1 and housekeeping control, HPRT1, transcript content (FIG. 19B). It was observed that pericytes derived from RCC tumors were uniquely enriched for DLK1 transcripts versus pericytes isolated from the animal-matched, tumor-uninvolved kidneys or VEC or RENCA cells (FIG. 19B). Immunofluorescence microscopy performed on day 21 RENCA tumor sections confirmed that DLK1 protein expression was associated with NG2⁺ pericytes but not CD31⁺ VEC in the tumor vasculature in situ (FIG. 19C).

Therapeutic Treatment of RENCA Tumor-Bearing Mice with a DLK1 Peptide-Based Vaccine is Effective and Associated with Specific Tc1 Activation and Recruitment into the TME.

The superior immunogenicity of a vaccine formulation composed of DC:IL12 pulsed with MHC class I-presented peptides to promote T helper-independent priming of specific CD8⁺ T cells (see above and Zhao et al., *J Immunol.* 2012; 188:1782-1788, Zhao et al., *Mol Ther.* 2012; 19:805-814). Using H-2^d class I-presented peptide epitopes derived from the murine DLK1 protein (i.e. DLK1₁₅₈₋₁₆₆, DLK1₁₆₁₋₁₆₉ and DLK1₂₅₉₋₂₇₀), the impact of treating BALB/c mice bearing established RENCA tumors with a DLK1 peptide-based vaccine was analyzed. As depicted in FIG. 20A, mice treated with the DLK1 peptide-based vaccines, but not the control vaccine (DC:IL12, no peptide) or PBS, exhibited a significant reduction in RENCA tumor growth (FIG. 20A; $p < 0.05$ (ANOVA) on days >13). On day 21 (i.e. 7 days after the booster immunization), CD8⁺ splenocytes were isolated and analyzed for their ability to produce IFN- γ in response to stimulation with specific DLK1 peptides in vitro. A superior level of IFN- γ secretion was observed from CD8⁺ T cells isolated from mice treated with the DC:IL12+DLK1 peptide vaccines (versus mice treated with DC:IL12 only or PBS) after stimulation with the individual DLK1 peptides (FIG. 20B).

A coordinate fluorescence microscopy analysis of tumor sections revealed that RENCA-bearing mice treated with the DLK1 peptide-based vaccine had fewer CD31⁺ blood vessels in the TME than control treatment cohorts, and these vessels contained VEC with an activated, VCAMV phenotype (FIG. 20C). RENCA tumors from DC:IL12+DLK1 peptide-treated mice contained abundant locoregional expression of the Tc1-recruiting chemokine CXCL10/IP-10 when compared to control tumors (FIG. 20D).

Vaccination with a Recombinant Lentivirus Encoding Murine DLK1 cDNA is Therapeutic in the RENCA Model.

Clinical trials implementing synthetic peptide-based vaccines are only applicable to subsets of cancer patients given the need to restrict accrual to individuals expressing relevant HLA class I (peptide-presenting) allotypes. The anti-tumor efficacy of a genetic vaccine was evaluated that would allow host antigen-presenting cells to process and present DLK1 peptides in a manner conducive to activate a broad anti-DLK1 (CD8⁺ and CD4⁺) T cell repertoire in any individual, regardless of their HLA type. Lentiviral-based vaccines promote prolonged antigen-specific CD8⁺ T cell responses after a

single administration in vivo (He et al. *Immunity.* 2006; 24:643-656). Thus, a recombinant lentivirus encoding full-length murine DLK1 (lvDLK1) and a negative control virus (lvNEG) was engineered.

To assess the therapeutic efficacy of specific genetic vaccination against the DLK1 antigen, RENCA-bearing mice were injected s.c. at a distal site with 40 TU or 200 TU of lvDLK1 or lvNEG in PBS. Animals injected with lvDLK1 at either dose exhibited significant reductions in tumor growth compared to animals treated with lvNEG (FIG. 21A). As was the case for the DLK1 peptide-based vaccine, immunofluorescence microscopy analysis of tumor sections supported decreased vascularity and loss of (DLK1⁺) vascular pericytes (FIG. 21B), and increased presence of VCAM1⁺CD31⁺ VEC and CXCL10 chemokine in the TME of mice treated with lvDLK1 versus lvNEG (FIG. 21C, 21D). Since VCAM1 and CXCL10 play important roles in the extravasation of recruited VLA-4⁺CXCR3⁺ Tc1 from blood into the TME (Bose et al., *Int J Cancer.* 2011; 129:2158-2170), levels of infiltrating CD8⁺ T cells in RENCA tumors were evaluated. As depicted in FIG. 21E, tumors isolated from mice treated with lvDLK1 contained greater numbers of CD8⁺ TIL.

Vaccination with a lvDLK1 Normalizes the RENCA Vasculature.

It has been suggested that in the absence of pericytes, the tumor vasculature appears "normalized," with lower densities of blood vessels and reduced vascular permeability in the TME (24), supporting therapeutic strategies designed to selectively reduce or eradicate vascular pericytes within sites of tumor. Given the ability of the lvDLK1-based genetic vaccine to reduce the content of DLK1⁺ cells in the tumor stroma, further evidence was sought supporting therapeutic vascular "normalization" as a consequence of treatment with the lvDLK1 genetic vaccine. It was initially noted that RENCA tumors harvested from mice treated with lvDLK1 appeared anemic when compared to control tumors (FIG. 22A). This subjective index was confirmed based on analysis of hemoglobin content in tumor lysates (FIG. 22A).

Tumors were analyzed for expression of NG2 (a general pericyte marker in both normal and tumor tissues; Stallcup, *J Neurocytol.* 2002; 31:423-435) using immunofluorescence microscopy, it was observed that animals receiving injections of lvDLK1 displayed tumors with significant reductions in NG2⁺ pericytes versus tumors from animals vaccinated with lvNEG (FIG. 22B, 22C). Residual tumor pericytes in lvDLK1-treated animals were tightly associated with CD31⁺ VEC, unlike the randomly-distributed pattern of pericytes detected in the stroma of tumors isolated from control mice (FIG. 22B, 22C). To investigate changes in vascular permeability, animals were labeled with two different dyes, lectin-FITC to bind the vascular endothelium and red 20 nm FLUOSPHERES® to determine vessel leakiness into tissue. When compared to controls, the tumor blood vessels in mice vaccinated with lvDLK1 displayed a simple tubular architecture devoid of extensive branching (FIG. 22D). Furthermore, while the perivascular stroma of tumors in control treated animals was littered with the red FLUOSPHERES®, these probes were virtually undetected in tumors harvested from lvDLK1 vaccinated mice, consistent with diminished vascular permeability in the TME of these latter animals (FIG. 22D). These data suggest that selective immunization against DLK1 allows for the immunotherapeutic "normalization" of tumor blood vessels in vivo.

Therapeutic Vaccination with lvDLK1 Results in Reduced Hypoxia and a Lower Incidence of Hypoxia-Responsive Cell Populations in the TME.

Hypoxia frequently occurs in solid tumors as a consequence of their “aberrant” blood vessels inefficiently perfusing oxygen into the TME (Matsumoto et al., *Proc Natl Acad Sci U.S.A.* 2009; 106:17898-17903; Jain, *Semin Oncol.* 2002; 29:3-9), resulting in reduced effector T cell (i.e. TIL) function, increased production of immunosuppressive modulators, dysregulated angiogenesis, and an accumulation of cancer stem cells (Wilson and Hay, *Nat Rev Cancer.* 2012; 11:393-410). To investigate changes in hypoxia within tumors after vaccination with lvDLK1 versus lvNEG, mice were injected i.p. with pimonidazole, which detects low [$<1.3\%$] O_2 tension (Levesque et al., *Stem Cells.* 2007; 25:1954-1965), and performed immunohistochemical analysis. Tumors isolated from mice receiving lvDLK1 vaccines had a very low hypoxic index when compared to tumors culled from control animals (FIG. 23A). Given this large difference in TME hypoxia post-vaccination with lvDLK1, the treatment impact on expression of molecules associated with vascular stromal cells (RGSS5) and/or cancer stem cells was investigated (Jarid1B aka histone demethylase lysine demethylase 5b; CD133, CD44), all hypoxia-responsive gene products (Roesch et al., *Cell.* 2010; 141:583-594; Liang et al., *BMC Cancer.* 2012; 12:201; Mathieu et al., *Cancer Res.* 2011; 71:4640-4652). Immuno-fluorescence microscopy analysis of day 27 tumors revealed that all of these markers were reduced in their abundance in the TME after vaccination with lvDLK1 (FIG. 23B-23E).

Therapeutic Vaccination with lvDLK1 Results in Increased Apoptosis of Tumor Cells Distal to Residual Blood Vessels in the Treated TME.

Given the trimming of vascular branches in the RENCA TME and reduction in vascular permeability after vaccination with lvDLK1 (but not lvNEG), it was hypothesized that plasma nutrients required for sustaining tumor cell viability would be limited to regions proximal to the residual, normalized blood vessel network. TUNEL analyses revealed that indeed, the level of cellular apoptosis in the TME of lvDLK1-treated mice was substantially increased when compared with tumors isolated from control treated animals (FIG. 24). Furthermore, virtually all apoptotic events in RENCA tumors isolated from lvDLK1-vaccinated mice were located in tissue regions distal (>60 microns) to residual CD31⁺ blood vessels (FIG. 24).

Thus, it has been documented that DLK1 is a tumor pericyte-associated antigen that can be immunologically targeted via specific peptide- or gene-based vaccination in vivo, leading to the effective “normalization” of the tumor vasculature and the TME. Effective therapeutic vaccination resulted in the activation of Type-1 (IFN- γ producing) DLK1-specific CD8⁺ T cells in the periphery (spleen) and the improved recruitment of CD8⁺ T cells into the TME with a focused localization around residual tumor blood vessels. After treatment with DLK1-based vaccines, the therapeutically-normalized blood vessels in RENCA tumors exhibited a simple conduit design with tightly-approximated (abluminal) DLK1-deficient pericyte populations and activated VCAM1⁺ VEC that appeared improved in their structural integrity based on reductions in vascular leakiness/permeability. As a consequence, progressively-growing RENCA tumors became normoxic after treatment with DLK1-based vaccines, with regions of the tumor mass that were distal to the residual normalized blood vessel network undergoing apoptotic death. Concomitantly, the CXCL10 chemokine responsible for recruiting Type 1 proinflammatory effector cells was dramatically upregulated only in DLK1-vaccinated mice, which coincided with improved accumulation of CD8⁺ TIL. These findings support a paradigm in which specific immune effec-

tor T cells may serve as regulators of the “angiogenic switch” by monitoring and controlling the status of DLK1⁺ pericytes within the TME.

Conditional activation of the Wnt/ β -catenin/NOTCH signaling pathway leads to vascular normalization (Reis et al. *J Exp Med.* 2012; 209:1611-1627), as indicated by reduced vascular density and improved mural cell attachment, in intracranial murine gliomas. Without being bound by theory, since DLK1 serves as a functional antagonist to NOTCH signaling (Falix et al., *Biochim Biophys Acta.* 2012; 1822: 988-995), its therapeutic removal from the TME as a consequence of DLK1-based vaccination in the present studies would be expected to lead to the de-repression of NOTCH signaling in RENCA tumors. As such, immune-mediated inhibition of DLK1 expression in the TME may represent a protector of NOTCH signaling, thereby maintaining the tumor angiogenic-switch in the “off” position (Leslie et al., *Development.* 2007; 134:839-844; Siekmann and Lawson, *Cell Adh Migr.* 2007; 1:104-106).

The therapeutically “normalized” TME post-vaccination with lvDLK1 was largely devoid of cell populations harboring stem-like phenotypes, regardless of whether such cells represented bona fide cancer stem cells or mesenchymal stem cells or alternate stem cell populations recruited into the TME. Without being bound by theory, the treatment-associated difference in tumor-associated stem cells could reflect the ability of vaccine-induced T cells to: i.) alter the supportive TME thereby limiting the recruitment, accumulation or expansion of such stem cell populations in the TME; ii.) promote the loss of hypoxia in the TME, leading to transcriptional silencing of stem cell markers, many of which have hypoxia-responsive elements (HRE) in their promoter regions (Liang et al., *BMC Cancer.* 2012; 12:201; Mathieu et al., *Cancer Res.* 2011; 71:4640-4652); iii.) promote the corollary cross-priming (Mathieu et al., supra) of specific immune responses against alternate tumor-associated stromal antigens (including stem cell antigens like Jarid1B, CD133 and CD44 among others) leading to specific stem cell regulation/eradication in vivo. Additionally, without being bound by theory, it is possible that stem cells are directly targeted by anti-DLK1 Tc1, since cells expressing DLK1 may also co-express stem cell markers, including CD133, c-kit, and SOX2 (Metsyanim et al., *PLoS One.* 2009; 4:e6709). Cancer stem cells employ many of the same signaling pathways as normal stem cells, including NOTCH (Takebe et al., *Nat Rev Clin Oncol.* 2011; 8:97-106); therefore, it is also feasible that effective silencing of DLK1 leads to a maturation event (and altered phenotypes) in stem cell populations within the TME. These mechanisms are clearly not mutually-exclusive and a combination of these may be involved in the biologic outcomes disclosed herein.

The anti-angiogenic action mediated by the DLK1 vaccine-induced CD8⁺ T cell repertoire would differ, and likely complement, that of alternative anti-angiogenic treatment modalities such as anti-VEGF antibodies (i.e. bevacizumab) and small molecule tyrosine kinase inhibitors (i.e. sunitinib) (Helfrich et al., *J Exp Med.* 2010; 207:491-503; Rini and Atkins, *Lancet Oncol.* 2009; 10:992-1000; Faivre et al., *Nat Rev Drug Discov.* 2007; 6:734-745). DLK1-based vaccines could represent a logical second-line approach in the many cases of developed resistance to bevacizumab or sunitinib. Pericytes freshly-isolated from human RCC (but not patient-matched normal adjacent kidney tissue) display differential DLK1 expression. DLK1-based vaccines can be used as treatment of patients with vascularized forms of cancer.

This example provides a clinical trial to study intradermal administration of α DC1s loaded with a mixture of six TBVA-derived peptides at the time of, or a cycle prior to, starting study treatment with the TKI dasatinib. Current therapeutic approaches available for patients with advanced-stage melanoma remain inadequate, and existing approaches including those involving immunotherapy with cytokines and/or targeted strategies have resulted in disappointingly low rates of durable and complete responses. Correcting immune dysfunction in advanced-stage melanoma patients using TKI such as dasatinib is proposed to relicense the patient's immune system to respond optimally to specific immunization. The integration of antigens expressed by tumor-associated blood vessel cells provides a means to selectively target the genetically-/antigenically-heterogeneous population of tumor cells in the advanced-stage melanoma patient.

CD8⁺ T cell responses are analyzed against the TBVA DLK1, EphA2, HBB, NRP1, RGS5, and TEM1 in peripheral blood of HLA-A2⁺ melanoma patients prior to, during the course of, and one month after the last dose of dasatinib. Based on the strong Type-1 polarizing potential of α DC1 in vitro, these vaccines enhance Type-1 CD8⁺ T cell responses against at least 3 of the 6 peptides included in the vaccine (particularly when patients receive concurrent dasatinib administration, as this removes the regulatory action of MDSC/Treg suppressor cells).

A mixture of six TBVA-derived epitopes is evaluated to be applied to α DC1s as an intradermal vaccine injection into 28 HLA-A2⁺ patients with advanced-stage melanoma. This choice is based on the finding of superior anti-tumor efficacy in HLA-A2 transgenic tumor models for the pooled peptide vaccine approach and the relevance of the TBVA-derived peptides (which share sequence identity in both human and mouse TBVA) in the HLA-A2⁺ human patient setting. The combinational vaccine+dasatinib modeling suggest that optimal therapeutic benefit against established M05 melanoma occurred when sunitinib administration was initiated at the time of initial vaccination or at the time of boosting.

Systemic review and meta-analysis of previous DC-based vaccine trials in cancer patients suggests that: i.) vaccine-induced T cell responses are associated with beneficial clinical outcome; ii.) mature DC (such as α DC1) were superior activators of specific immunity and a better clinical prognosis when compared to immature DC; iii.) while a threshold dose of DC is required in the vaccine in order to promote specific immunity, a vast increase in DC number over that threshold did not generally yield superior efficacy (Eggert et al., *Cancer Res.* 1999; 59: 3340-3345; Linette et al., *Clin Cancer Res.* 2005; 11: 7692-7699; Verdijk et al., *Clin Cancer Res.* 2009; 15: 2531-2540; Lesterhuis et al., *Clin Cancer Res.* 2011; July 19 [Epub ahead of print]; Castiglione and Piccoli, *J Theor Biol.* 2007; 247: 723-732; Draube et al., *PLoS One.* 2011; 6: e18801). A recent study by Verdijk et al. suggests that intradermal delivery of DC-based vaccines in patients with advanced stage melanoma was clinically equitable to the delivery of these cells directly into lymph nodes (Verdijk et al., op. cit.), while a report from Lesterhuis and colleagues argues that intradermal delivered DC-based vaccines were superior to intranodal delivered vaccines in promoting melanoma-specific T cell activation in vivo (Lesterhuis et al., op cit.). In vivo tracking of intradermal injected DC in melanoma patients suggests that approximately 4% of the administered DC actually migrate to tissue-draining lymph nodes and that

the delivery of approximately 5×10^5 (vaccine) DC are needed to promote clinically-meaningful levels of antigen-specific T cells (Verdijk et al., op. cit.). By extrapolation, these figures indicate that intradermal injection of a vaccine containing approximately 10^7 mature antigen-loaded α DC1 would be anticipated to provide a quasi-optimal degree of immune stimulation that may be associated with clinical benefit. Pre-clinical, clinical, and mathematical modeling all suggest that optimal vaccine-induced immunity and benefit to the tumor-bearing host can be best achieved through repeated immunization (3-5 vaccines) provided over a regular-interval schedule. Since there is no consensus in the literature for an optimal time interval between the individual vaccinations, a protocol was adopted involving 4 intradermal vaccines every 2 weeks, which is a commonly employed schedule for DC-based vaccines (Lesterhuis et al., op cit.).

A single-center, prospective randomized, pilot, Phase 2 trial is conducted evaluating the activity, safety and immune effects of dasatinib given in combination with an autologous type-1 polarized DC vaccine. Dasatinib is administered at the standard dose and schedule recommended by the FDA (70 mg BID). The autologous type-I DC vaccine is administered either prior to, or concomitant with, the initiation of dasatinib administration. Patients are vaccinated intradermally with the α DC1/peptide mixture on days 1 and 15 of every cycle on an outpatient basis. For those patients starting therapy with vaccine alone, dasatinib is initiated on day 29 after receiving the first immunization. Unless patients are removed from study, they are treated for at least 6 cycles or disease progression. In cases where there is continued clinical benefit and no additional vaccine product is available, patients can continue to be treated on single agent dasatinib.

Leukapheresis

Leukapheresis (90 minutes) is a minimal risk procedure. Prior to the procedure each subject's venous access is evaluated. If a subject does not have acceptable venous access a pheresis catheter is put in place. All selected patients undergo a single 90 minute-long limited leukapheresis once they have been deemed eligible and prior to the first course of vaccination. One time of the subject's blood volume is processed per procedure.

Leukapheresed product is immediately, and a part of it is used for the first vaccination course (Week 1). The remainder of the product is cryopreserved as described. If cytopenia ($WBC < 2000/mm^3$ or platelets $< 40,000/mm^3$) develops during, or as a result of, leukapheresis, the procedure is postponed until recovery. This will not be considered an adverse event. Samples from each cell product are obtained for hemoglobin, hematocrit, total WBC, and differential and platelet count.

Vaccine

Formulation

Dendritic cells (DC) are derived from autologous (the subject's own) adherent mononuclear cells (monocytes) in the peripheral blood obtained from leukapheresis. In this case, "biologic product" and "biologic substance" are the same.

Storage and Preparation

The final product is placed in vials with labels identifying each unique vaccine lot and cryopreserved. DCs used in the vaccine are suspended in 5% human serum albumin (HSA) and delivered to the clinic for administration. For preparation of the vaccines, the labeled vials of cryopreserved α DC1 are

removed from storage in liquid nitrogen and quickly thawed in a 37° C. water bath. After 3 washes in sterile medium, thawed αDC1 are suspended in saline with 5% human serum albumin (HSA), placed in sterile syringes for administration to the subject and delivered to the clinic for administration. Each syringe is labeled with a custom-designed label, identifying the subject and the vaccine. Both saline and HSA are clinical grade.

Administration

The autologous type-I DC vaccine are administered intradermally either prior to, or concomitant with, the initiation of dasatinib administration. The injections are performed on an outpatient basis.

Dendritic cell-based vaccines have been extensively evaluated in thousands of cancer patients over the past 15 years) and found to be safe and extremely well-tolerated.

Study Treatment Plan

No investigational or commercial agents or therapies other than those described below are administered with the intent to treat the patient's malignancy.

Dasatinib Administration

All patients receive dasatinib at a starting dose of 70 mg twice daily by mouth in the outpatient setting. Dasatinib is supplied as 50 mg and 20 mg tablets. Patients take 1 of the 50 mg tablets and 1 of the 20 mg tablets twice daily, approximately every 12 hours, at the same time each day. Dasatinib may be taken with or without food. Patients swallow the tablets whole.

Patients on Arm A start dasatinib administration on cycle 2, day 1 (week 5), while those patients in Arm B start dasatinib administration on cycle 1, day 1 (week 1). Study treatment continues for at least 6 cycles or disease progression. In case of vaccine depletion patients may continue on dasatinib alone and there is evidence of clinical benefit.

The dosing time is adjusted as required for subject convenience. If doses are missed for toxicity, they are not replaced. If a dose is not taken due to an error, it may be taken up to 12 hours later. If vomiting occurs within 30 minutes of intake, that dose is repeated.

REGIMEN DESCRIPTION						
	Agent	Premedications/ Precautions	Dose	Route	Schedule	Cycle Length
5	α DC1 Vaccine	None	10^7 cells	Intra-dermal injection	Arms A and B: every 2 weeks starting on Cycle 1, day 1	28 days (4 weeks)
10	Dasatinib	Take with or without food	70 mg	Orally, twice a day	Arm A: Daily starting on Cycle 2, day 1 Arm B: daily starting on Cycle 1, day 1	

Vaccine Administration

The DC vaccine is administered by a single intradermal injection of approximately 10^7 cells (a minimum of 5×10^6 cells is allowable due to manufacturing limitations), with all the DCs being administered on days 1 and 15 of each cycle. The intradermal administration is in the vicinity of the four nodal drainage groups of the four extremities and performed on an outpatient basis. Study treatment will continue for at least 6 cycles or disease progression.

25 Duration of Study Treatment

In the absence of treatment delays due to adverse events, treatment continues for at least 6 cycles until one of the following criteria applies: Disease progression, Intercurrent illness that prevents further administration of treatment, Unacceptable adverse event(s), Patient decides to withdraw from the study, or General or specific changes in the patient's condition render the patient unacceptable for further treatment in the judgment of the investigator/sub-investigator, Study is terminated, or Loss of ability to freely provide consent

35 Duration of Follow Up

Patients are followed for 1 year after removal from study or until death, whichever occurs first.

Study Calendar

Schedules Shown in the Study Calendar Below are Provided
40 as an Example and should be Modified as Appropriate.

Baseline evaluations are conducted within 1 week prior to start of protocol therapy. Scans and x-rays are done ≤ 4 weeks prior to the start of therapy. In the event that the patient's condition is deteriorating, laboratory evaluations are repeated within 48 hours prior to initiation of the next cycle of therapy.

[illegible]

-continued

	Week									Off Study Treatment/	
	Up to -4 ^d	1	2	3	4	5	6	7	8		
Dasatinib											
Arm A						X	X	X	X		
Arm B		X	X	X	X	X	X	X	X		
DC Vaccine		X		X		X		X			
Immune monitoring- PBMC	X		X		X		X		X	X	
Tumor Biopsy	X					X					
AE evaluation					← X →					X	
Tumor measurements	X	Tumor measurements are repeated every 8 weeks. Documentation (radiologic) must be provided for patients removed from study for progressive disease.									X
Radiologic evaluation	X	Radiologic measurements should be performed every 8 weeks.									X ^g

^aNot necessary if already known;^bAlbumin, alkaline phosphatase, total bilirubin, bicarbonate, BUN, calcium, chloride, creatinine, glucose, LDH, phosphorus, potassium, total protein, SGOT [AST], SGPT [ALT], sodium, magnesium;^cSerum pregnancy test (women of childbearing potential);^dScreening is to be performed in the UPCL-CTRC;^eTreatment with DC vaccine and dasatinib will continue for at least 6 cycles (or until disease progression), the weeks of those cycles will follow the tests and procedures listed for weeks 5 through 8 above for each subsequent cycle;^fFour weeks after the last dasatinib administration;^gIf removed from the study for reasons other than DP.

Dose-Limiting Toxicities

Definition of Dose-Limiting Toxicity

Toxicities are scored according to the NCI Common Terminology Criteria for Adverse Events (NCI CTCAE) v4.0.

Dose-limiting toxicity (DLT) is defined as the following study drug-related events experienced during Cycle 1:

Grade 4 neutropenia or thrombocytopenia which lasts more than 7 days;

Grade 3 or 4 febrile neutropenia; or

Grade 3 or greater non-hematological toxicities; this includes grade 3 or greater diarrhea, nausea or vomiting which last more than 7 days despite adequate treatment (with loperamide for diarrhea, 5HT3 antagonists, steroids and dopamine antagonist for NN).

Dasatinib Dosing Delays/Modifications

Dose Level	Dasatinib Dose
0	70 mg BID
-1	50 mg BID
-2	100 mg QD

The study uses the CTCAE (Common Terminology Criteria for Adverse Events) version 4.0 for toxicity and serious adverse event reporting.

Patient Selection

Inclusion Criteria

Patients are HLA-A2⁺ and have histologically confirmed melanoma that is metastatic (Stage IV) or unresectable Stage IIIB/C and for which standard curative or palliative measures do not exist or are no longer effective.

Patients have measurable disease by RECIST 1.1, defined as at least one lesion that can be accurately measured in at least one dimension (longest diameter to be recorded for non-nodal lesions and short axis for nodal lesions) as ≥ 20 mm with conventional techniques or as ≥ 10 mm with spiral CT scan, MRI, or calipers by clinical exam.

Patients have at least 2 subcutaneous, intracutaneous, and accessible tumor deposits, lymph node or other site available for biopsy purposes.

Prior chemotherapy, immunotherapy, or targeted therapy is allowed as long as it did not include dasatinib.

Age ≥ 18 years. Because no dosing or adverse event data are currently available on the use of dasatinib in patients < 18 years of age, children are excluded.

ECOG performance status ≤ 2 (Karnofsky $\geq 60\%$)

Life expectancy of greater than 12 weeks.

Patients have normal organ and marrow function as defined below:

Leukocytes $\geq 3,000/\mu\text{L}$

absolute neutrophil count $\geq 1,500/\mu\text{L}$

absolute lymphocyte count $\geq 500/\mu\text{L}$

platelets $\geq 100,000/\mu\text{L}$

total bilirubin within normal institutional limits

AST(SGOT)/ALT(SGPT) $\leq 2.5 \times$ institutional upper limit of normal

Creatinine $\leq 2.0 \times$ institutional upper limit of normal

Serum magnesium, potassium and adjusted (or ionized) calcium \geq the institutional lower limit of normal. (Supplementation of electrolytes prior to screening is allowed).

Sexually active women and men of childbearing potential agree to use an effective method of birth control during the course of the study and for up to 3 months following the last dose of the study drug, in a manner such that risk of pregnancy is minimized. Surgical sterilization, intrauterine device or barrier method (e.g. condom and/or diaphragm with spermicidal agents) are acceptable forms of birth control. Women of childbearing potential have a negative pregnancy test (serum) within 7 days prior to treatment. A pregnancy test is not required for registration. Women who have not menstruated for more than 2 years are considered postmenopausal, thus not of childbearing potential.

Exclusion Criteria

Patients who have had chemotherapy or radiotherapy within 4 weeks (6 weeks for nitrosoureas or mitomycin C) prior to entering the study or those who have not recovered from adverse events due to agents administered more than 4 weeks earlier.

Patients with documented c-KIT mutations.

Patients who are receiving any other investigational agents. Patients with known brain metastases should be excluded from this clinical trial because of their poor prognosis and because they often develop progressive neurologic dysfunction that would confound the evaluation of neurologic and other adverse events.

History of allergic reactions attributed to compounds of similar chemical or biologic composition to dasatinib or any of the components of the vaccine being administered as part of this study.

Women who are pregnant or nursing/breastfeeding.

History of significant bleeding disorder unrelated to cancer, including:

- Diagnosed congenital bleeding disorders (e.g., von Willebrand's disease)
- Diagnosed acquired bleeding disorder within one year (e.g., acquired anti-factor VIII antibodies)

Patients currently taking medications that inhibit platelet function (i.e., aspirin, dipyridamole, epoprostenol, eptifibatide, clopidogrel, cilostazol, abciximab, ticlopidine, and any non-steroidal anti-inflammatory drug) because of a potential increased risk of bleeding from dasatinib.

Patients currently taking anticoagulants (warfarin, heparin/low molecular weight heparin [e.g., danaparoid, dalteparin, tinzaparin, enoxaparin]) because of a potential increased risk of bleeding from dasatinib.

Diagnosis of unstable angina or myocardial infarction within 6 months of study entry.

Patients currently taking one or more of the following drugs that are generally accepted to have a risk of causing Torsades de Pointes:

- quinidine, procainamide, disopyramide
- amiodarone, sotalol, ibutilide, dofetilide
- erythromycins, clarithromycin
- chlorpromazine, haloperidol, mesoridazine, thioridazine, pimozide
- cisapride, bepridil, droperidol, methadone, arsenic, chloroquine, domperidone, halofantrine, levomefentanyl, pentamidine, sparfloxacin, lidoflazine.

Diagnosed or suspected congenital long QT syndrome.

Prolonged QTc interval on pre-entry electrocardiogram (>450 msec) within 30 days prior to study registration.

Any history of clinically significant ventricular arrhythmias (such as ventricular tachycardia, ventricular fibrillation, or Torsades de pointes)

Uncontrolled intercurrent illness including, but not limited to, ongoing or active infection, symptomatic congestive heart failure, unstable angina pectoris, cardiac arrhythmia, or psychiatric illness/social situations that would limit compliance with study requirements.

HIV-positive patients on combination antiretroviral therapy are ineligible because of the potential for pharmacokinetic interactions with dasatinib. In addition, these patients are at increased risk of lethal infections when treated with marrow-suppressive therapy. Appropriate studies are undertaken in patients receiving combination antiretroviral therapy when indicated.

Research Samples

Patient peripheral blood and tumor biopsies are obtained at various time points prior to, and after, the initiation of therapy. If the patient is determined to express the HLA-A2 antigen on their peripheral blood cells, to express a wild-type phenotype, and they pass all additional inclusion/exclusion criteria, after written consent, they are entered on trial. Those patients determined to express c-KIT mutations are excluded from study, while BRAF mutational status is used to stratify

patients during randomization to ensure a balanced proportion of patients with the mutation on both arms.

Biopsy Tissue.

Melanoma biopsies are obtained prior to the first vaccination (baseline) and week 5 (date of the third vaccination). Patients should have at least 2 subcutaneous, intracutaneous, and accessible tumor deposits, lymph node or other site available for biopsy purposes.

Blood Samples

At least 3 weeks prior to study treatment, peripheral blood is obtained for the screening of patient HLA-A2 expression status and for baseline testing. Peripheral blood is obtained every 2 weeks on trial beginning week 2.

Correlative Studies

HLA-A2/TBVA peptide dextramer⁺ CD8⁺ T cells (i.e. CD8⁺ T cells imaged by flow cytometry using a fluorescently-labeled, antigen-specific probe) exhibits higher frequencies in the peripheral blood and a greater propensity to produce IFN- γ after the initiation of α DC1-based vaccines. Since dasatinib alters the recruiting capacity of the tumor microenvironment based on activation of VCAM-1 expression on the tumor-associated vascular endothelial cells and locoregional production of CXCR3 ligand chemokines, the frequency of TBVA-specific CD8⁺ T cells selectively declines in the patients peripheral blood if the combined therapy performs as expected. Circulating levels of the CXCR3 ligand CXCL10 (aka IP-10), become elevated under treatment conditions in patients that are more prone to exhibit objective clinical response to effective immunotherapy. As a consequence, levels of serum CXCL10 are analyzed before, during and after combined vaccine+dasatinib therapy to determine correlation with TBVA-specific CD8⁺ T cells in the blood versus tumor over time post-treatment.

Immune Monitoring Analysis of TBVA-Specific CD8⁺ T Cell Responses (Primary Endpoint).

Rationale and Hypothesis:

Translation and clinical vaccine trials have demonstrated that DC/peptide-based vaccines effectively activate specific CD8⁺ T cells in tumor-bearing hosts that may be detected in peripheral blood, and that individuals that exhibit objective clinical response to such vaccine therapies tend to derive from the cohort of patients that display detectable increases in T cell responses post-vaccination (see, for example, Keiholz, *Recent Results Cancer Res.* 2007; 176: 213-218). The effectiveness of DC1/peptide vaccination to elicit protective/therapeutic T cell-mediated immunity in melanoma models in vivo (see above), support the hypothesis that α DC1/peptide vaccination of advanced stage melanoma patients results in increased quantities of specific CD8⁺ T cells in patient peripheral blood and that those individuals in which improved response to many peptides can be observed are those that are more likely to demonstrate clinical benefit.

Method:

Using fluorescently-labeled HLA-A2/peptide dextramer probes and intracellular staining for the Type-1 cytokine IFN- γ , how the frequency of CD8⁺ T cells specific for TBVA peptides changes over time post-vaccination and how many of these T cells are Type-1 effector T cells is determined. Quantitation of CD8⁺ T cells, Treg, MDSC and Blood Vessels in Melanoma Biopsy Tissue

Rationale and Hypothesis:

Without being bound by theory, tumor progression is believed to be linked to the accumulation of suppressor cell populations (both MDSC and Treg) and strong pro-angiogenic signals, as well as, "prevention" of Type-1 T cell recruitment within the tumor microenvironment (see, for example, Wolf et al., *Clin Cancer Res.* 2005; 11: 8326-8331).

The data in murine melanoma models support the ability of dasatinib (particularly when combined with DC1/peptide vaccines) to counteract these biologic endpoints in vivo. These changes may also be evidenced in effectively treated melanoma patients by analyzing melanoma biopsies taken post- versus pre-treatment and that the greatest "normalization" of the tumor microenvironment is observed after treatment with combined dasatinib+vaccine therapy.

Method:

Immunofluorescence microscopy is used to analyze tumor sections of melanoma biopsies for expression of the markers CD8 α (T effector cells), CD11b+CD33+lack of HLA-DR (lineage-negative MDSC), CD11b+CD15+lack of CD14 (neutrophilic MDSC), CD11b+CD14+lack of CD15 (myeloid MDSC), CD4+Foxp3 (Treg cells) and CD31+NG2 (blood vessels). After staining and washing, sections are covered in Gelvatol (Monsanto, St. Louis, Mo.) and a coverslip applied. Positively-stained cells are quantitated by analyzing the images at a final magnification of $\times 20$ using Metamorph Imaging software (Molecular Devices, Sunnyvale, Calif.).

Treg Analysis in PBMC

Rationale and Hypothesis:

Cancer patients have commonly also been shown to have elevated populational frequencies of Treg (based on the CD4⁺ Foxp3⁺ phenotype) circulating in their peripheral blood. Alternate TKI, such as sunitinib, have been shown capable of reducing peripheral blood Treg levels within the first 4 week cycle of drug administration, in concert with a rebound in Type-1 T cell numbers and function in PBMC (Finke et al., *Clin Cancer Res.* 2008; 14: 6674-6682). Dasatinib provides a similar effect in melanoma patients and that those patients exhibiting the greatest degree of Treg reduction post-therapy respond favorably against the peptide epitopes contained in the vaccine formulation.

Method:

Peripheral blood cells are analyzed by flow cytometry using specific antibodies against CD3 (all T cells), CD4⁺ Foxp3 (Treg), CD4⁺CD25^{hi} (Treg). Results are expressed as percentage of CD25^{hi}/Foxp3⁺ cells out of total CD3⁺/CD4⁺ viable cells.

MDSC Analysis in PBMC

Rationale and Hypothesis:

Similar to Treg, levels of cells expressing an MDSC phenotype have been reported to be elevated in the peripheral blood of cancer patients, including patients with advanced-stage melanoma (see, for example, Ko et al., *Clin Cancer Res.* 2009; 15: 2148-2157). TKI, such as sunitinib and dasatinib can reduce the frequency of such suppressor cells to a variable degree when used as a therapy. Melanoma patients treated with dasatinib exhibit reduction in MDSC frequencies in PBMC, with the degree of loss correlating with the patient's ability to respond favorably against the peptide epitopes contained in the vaccine formulation.

Method:

Analysis of MDSC percentages in patient PBMC is performed using flow cytometry and anti-human antibodies against CD11b, CD11c, CD14, CD15, CD33 and HLA-DR. EphA2 Protein Levels in Tumor Biopsies

Rationale and Hypothesis:

Drug treatments (including dasatinib in vitro) that promote the proteasome-dependent degradation of the tumor (and tumor vascular endothelial) cell-associated protein EphA2 lead to improved recognition by specific CD8⁺ T cells (see, for example, Kawabe et al., *Cancer Res.* 2009; 69: 6995-7003). Administration of dasatinib to melanoma patients promotes the loss of EphA2 protein within the tumor lesion, leading to an enhancement in the sensitivity of EphA2⁺ cells

in the tumor microenvironment to EphA2-specific CD8⁺ T cells that have been activated as a consequence of α DC1/peptide-based vaccination.

Method:

Western blotting and immunofluorescence microscopy are used to quantitate EphA2 protein expression in melanoma biopsies pre- versus post-vaccination.

CXCL10 Levels in Patient Serum

Rationale and Hypothesis:

Therapeutic CD8⁺ T cells require the production of CXCR3 ligand chemokines within the tumor microenvironment in order to effectively home to these disease sites. Two recent clinical trials, including a α DC1/glioma peptide vaccination trial in patients with brain tumors strongly support CXCL10 (aka IP-10) as a chemokine associated with superior clinical outcome to immune-based therapy (see, for example, Schwaab et al., *Clin Cancer Res.* 2009; 15: 4986-4992). This will also be the case in the α DC1/TBVA peptide vaccinated patients with melanoma where Type-1 CXCR3⁺ responder T cells require a gradient of CXCL10/IP-10 (as detected in serum) in order to traffick to tumor sites in vivo.

Method: Patient serum levels of CXCL10 are monitored using Luminex fluorescent bead technology according to manufacturer's protocol.

Measurement of Effect

Patients with measurable disease are assessed by standard criteria. Patients are re-evaluated every 8 weeks. In addition to a baseline scan, confirmatory scans are obtained ≥ 4 weeks following initial documentation of an objective response.

Antitumor Effect

Patients are re-evaluated for response every 8 weeks. In addition to a baseline scan, confirmatory scans are obtained no less than 4 weeks following initial documentation of objective response.

Response and progression are evaluated using the new international criteria proposed by the revised Response Evaluation Criteria in Solid Tumors (RECIST) guideline (version 1.1; ref. 104). Changes in the largest diameter (unidimensional measurement) of the tumor lesions and the shortest diameter in the case of malignant lymph nodes are used in the RECIST criteria.

Definitions

Evaluable for toxicity. All patients are evaluable for toxicity from the time of their first treatment.

Evaluable for objective response. Only those patients who have measurable disease present at baseline, have received at least one cycle of therapy, and have had their disease re-evaluated are considered evaluable for response. These patients have their response classified according to the definitions stated below. (Note: Patients who exhibit objective disease progression prior to the end of cycle 1 will also be considered evaluable.)

Evaluable Non-Target Disease Response. Patients who have lesions present at baseline that are evaluable but do not meet the definitions of measurable disease, have received at least one cycle of therapy, and have had their disease re-evaluated are considered evaluable for non-target disease. The response assessment is based on the presence, absence, or unequivocal progression of the lesions.

Disease Parameters

Measurable disease. Measurable lesions are defined as those that can be accurately measured in at least one dimension (longest diameter to be recorded) as ≥ 20 mm by chest x-ray or as ≥ 10 mm with CT scan, MRI, or calipers by clinical exam. All tumor measurements must be recorded in millime-

ters (or decimal fractions of centimeters). Tumor lesions that are situated in a previously irradiated area might or might not be considered measurable.

Malignant lymph nodes. To be considered pathologically enlarged and measurable, a lymph node must be ≥ 15 mm in short axis when assessed by CT scan (CT scan slice thickness recommended to be no greater than 5 mm) At baseline and in follow-up, only the short axis is measured and followed.

Non-measurable disease. All other lesions (or sites of disease), including small lesions (longest diameter < 10 mm or pathological lymph nodes with ≥ 10 to < 15 mm short axis), are considered non-measurable disease. Bone lesions, leptomeningeal disease, ascites, pleural/pericardial effusions, lymphangitis cutis/pulmonitis, inflammatory breast disease, and abdominal masses (not followed by CT or MRI), are considered as non-measurable. Cystic lesions that meet the criteria for radiographically defined simple cysts are not be considered as malignant lesions (neither measurable nor non-measurable) since they are, by definition, simple cysts. 'Cystic lesions' thought to represent cystic metastases can be considered as measurable lesions, if they meet the definition of measurability described above. However, if non-cystic lesions are present in the same patient, these are preferred for selection as target lesions.

Target lesions. All measurable lesions up to a maximum of 2 lesions per organ and 5 lesions in total, representative of all involved organs, should be identified as target lesions and recorded and measured at baseline. Target lesions are selected on the basis of their size (lesions with the longest diameter), are representative of all involved organs, but in addition lend themselves to reproducible repeated measurements. It may be the case that, on occasion, the largest lesion does not lend itself to reproducible measurement in which circumstance the next largest lesion which can be measured reproducibly is selected. A sum of the diameters (longest for non-nodal lesions, short axis for nodal lesions) for all target lesions is calculated and reported as the baseline sum diameters. If lymph nodes are included in the sum, then only the short axis is added into the sum. The baseline sum diameters are used as reference to further characterize any objective tumor regression in the measurable dimension of the disease.

Non-target lesions. All other lesions (or sites of disease) including any measurable lesions over and above the 5 target lesions are identified as non-target lesions and are recorded at baseline. Measurements of these lesions are not required, but the presence, absence, or in rare cases unequivocal progression of each is noted throughout follow-up.

Methods for Evaluation of Measurable Disease

All measurements are taken and recorded in metric notation using a ruler or calipers. All baseline evaluations are performed as closely as possible to the beginning of treatment and never more than 4 weeks before the beginning of the treatment.

The same method of assessment and the same technique is used to characterize each identified and reported lesion at baseline and during follow-up. Imaging-based evaluation is preferred to evaluation by clinical examination unless the lesion(s) being followed cannot be imaged but are assessable by clinical exam.

Clinical lesions. Clinical lesions are only considered measurable when they are superficial (e.g., skin nodules and palpable lymph nodes) and ≥ 10 mm diameter as assessed using calipers (e.g., skin nodules). In the case of skin lesions they are documented by color photography, including a ruler to estimate the size of the lesion.

Chest x-ray. Lesions on chest x-ray are measurable lesions when they are clearly defined and surrounded by aerated lung, but CT is preferable.

Conventional CT and MRI. This guideline has defined measurability of lesions on CT scan based on the assumption that CT slice thickness is 5 mm or less. If CT scans have slice thickness greater than 5 mm, the minimum size for a measurable lesion should be twice the slice thickness. MRI is also acceptable in certain situations (e.g. for body scans). MRI has excellent contrast, spatial, and temporal resolution. As with CT, if an MRI is performed, the technical specifications of the scanning sequences used are optimized for the evaluation of the type and site of disease. Furthermore, as with CT, the modality used at follow-up is the same as was used at baseline and the lesions are measured/assessed on the same pulse sequence.

PET-CT. The low dose or attenuation correction CT portion of a combined PET-CT is not always of optimal diagnostic CT quality for use with RECIST measurements. However, if the CT performed as part of a PET-CT is of identical diagnostic quality to a diagnostic CT (with IV and oral contrast), then the CT portion of the PET-CT can be used for RECIST measurements and can be used interchangeably with conventional CT in accurately measuring cancer lesions over time.

Endoscopy, Laparoscopy. Such techniques are used to confirm complete pathological response when biopsies are obtained or to determine relapse in trials where recurrence following complete response (CR) or surgical resection is an endpoint.

Cytology, Histology. These techniques can be used to differentiate between partial responses (PR) and complete responses (CR) in rare cases (e.g., residual lesions in tumor types, such as germ cell tumors, where known residual benign tumors can remain). The cytological confirmation of the neoplastic origin of any effusion that appears or worsens during treatment when the measurable tumor has met criteria for response or stable disease is mandatory to differentiate between response or stable disease (an effusion may be a side effect of the treatment) and progressive disease.

FDG-PET. FDG-PET response assessments can be incorporated to complement CT scanning in assessment of progression (particularly possible 'new' disease). New lesions on the basis of FDG-PET imaging are identified according to the following algorithm:

Negative FDG-PET at baseline, with a positive FDG-PET at follow-up is a sign of PD based on a new lesion.

No FDG-PET at baseline and a positive FDG-PET at follow-up: If the positive FDG-PET at follow-up corresponds to a new site of disease confirmed by CT, this is PD. If the positive FDG-PET at follow-up is not confirmed as a new site of disease on CT, additional follow-up CT scans are needed to determine if there is truly progression occurring at that site (if so, the date of PD is the date of the initial abnormal FDG-PET scan). If the positive FDG-PET at follow-up corresponds to a pre-existing site of disease on CT that is not progressing on the basis of the anatomic images, this is not PD.

FDG-PET may be used to upgrade a response to a CR in a manner similar to a biopsy in cases where a residual radiographic abnormality is thought to represent fibrosis or scarring. The use of FDG-PET in this circumstance should be prospectively described in the protocol and supported by disease-specific medical literature for the indication. However, it must be acknowledged that both approaches may lead to false positive CR due to limitations of FDG-PET and biopsy resolution/sensitivity.

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Note: A 'positive' FDG-PET scan lesion means one which is FDG avid with an uptake greater than twice that of the surrounding tissue on the attenuation corrected image.

Response Criteria

Evaluation of Target Lesions

Complete Response (CR): Disappearance of all target lesions. Any pathological lymph nodes (whether target or non-target) must have reduction in short axis to <10 mm.

Partial Response (PR): At least a 30% decrease in the sum of the diameters of target lesions, taking as reference the baseline sum diameters.

Progressive Disease (PD): At least a 20% increase in the sum of the diameters of target lesions, taking as reference the smallest sum on study (this includes the baseline sum if that is the smallest on study). In addition to the relative increase of 20%, the sum must also demonstrate an absolute increase of at least 5 mm (Note: the appearance of one or more new lesions is also considered progressions).

Stable Disease (SD): Neither sufficient shrinkage to qualify for PR nor sufficient increase to qualify for PD, taking as reference the smallest sum diameters while on study.

Evaluation of Non-Target Lesions

Complete Response (CR): Disappearance of all non-target lesions and normalization of tumor marker level. All lymph nodes must be non-pathological in size (<10 mm short axis).

Note: If tumor markers are initially above the upper normal limit, they must normalize for a patient to be considered in complete clinical response.

Non-CR/Non-PD: Persistence of one or more non-target lesion(s) and/or maintenance of tumor marker level above the normal limits.

Progressive Disease (PD): Appearance of one or more new lesions and/or unequivocal progression of existing non-target lesions. Unequivocal progression should not normally trump target lesion status. It must be representative of overall disease status change, not a single lesion increase.

Evaluation of Best Overall Response

The best overall response is the best response recorded from the start of the treatment until disease progression/recurrence (taking as reference for progressive disease the smallest measurements recorded since the treatment started). The patient's best response assignment depends on the achievement of both measurement and confirmation criteria.

For Patients with Measurable Disease (i.e., Target Disease)

Target Lesions	Non-Target Lesions	New Lesions	Overall Response	Best Overall Response when Confirmation is Required*
CR	CR	No	CR	≥4 wks. Confirmation**
CR	Non-CR/Non-PD	No	PR	≥4 wks. Confirmation**
CR	Not evaluated	No	PR	
PR	Non-CR/Non-PD/ not evaluated	No	PR	
SD	Non-CR/Non-PD/not evaluated	No	SD	Documented at least once ≥4 wks. from baseline**
PD	Any	Yes or No	PD	no prior SD, PR or CR

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Target Lesions	Non-Target Lesions	New Lesions	Overall Response	Best Overall Response when Confirmation is Required*
Any	PD***	Yes or No	PD	
Any	Any	Yes	PD	

*See RECIST 1.1 manuscript for further details on what is evidence of a new lesion.

**Only for non-randomized trials with response as primary endpoint.

10 ***In exceptional circumstances, unequivocal progression in non-target lesions may be accepted as disease progression.

Note:

Patients with a global deterioration of health status requiring discontinuation of treatment without objective evidence of disease progression at that time should be reported as "symptomatic deterioration." Every effort should be made to document the objective progression even after discontinuation of treatment.

15 For Patients with Non-Measurable Disease (i.e., Non-Target Disease)

Non-Target Lesions	New Lesions	Overall Response
CR	No	CR
Non-CR/non-PD	No	Non-CR/non-PD*
Not all evaluated	No	not evaluated
Unequivocal PD	Yes or No	PD
Any	Yes	PD

25 **Non-CR/non-PD* is preferred over 'stable disease' for non-target disease since SD is increasingly used as an endpoint for assessment of efficacy in some trials so to assign this category when no lesions can be measured is not advised

Duration of Response

Duration of Overall Response:

30 The duration of overall response is measured from the time measurement criteria are met for CR or PR (whichever is first recorded) until the first date that recurrent or progressive disease is objectively documented (taking as reference for progressive disease the smallest measurements recorded since the treatment started).

35 The duration of overall CR is measured from the time measurement criteria are first met for CR until the first date that progressive disease is objectively documented.

Duration of Stable Disease:

40 Stable disease is measured from the start of the treatment until the criteria for progression are met, taking as reference the smallest measurements recorded since the treatment started, including the baseline measurements.

Progression-Free Survival

45 Progression-free survival (PFS) is defined as the duration of time from start of treatment to time of progression or death, whichever occurs first.

Statistical Considerations

Study Design

50 The effects of combination therapy of dasatinib and vaccine on immune response rate are evaluated. A patient who responded to at least 3 of the 6 peptides is considered to have a positive immune response. The secondary objectives include evaluation of clinical response rate, overall survival (OS), progression free survival (PFS), and immunological endpoints, which include number of CD8⁺ T cells, MDSC/Treg regulatory cells and blood vessels in tumor lesions, level of EphA2 protein expressed within the tumor lesion and the level of the CXCL10/IP-10 chemokine in patient serum pre-versus post-treatment.

Up to 28 evaluable patients are randomized in 1:1 ratio to receive either:

65 A. Vaccine alone starting in the first 28-day cycle followed by vaccine combined with daily dasatinib starting on the first day of the second cycle (Arm A)

85

B. Vaccine combined with daily dasatinib starting on the first day of cycle 1 (Arm B)

Patients not evaluable for immune response are replaced. Randomization is stratified by BRAF mutation status.

Data Analysis

Analysis Sets.

Evaluable Patients are patients who meet all of the protocol inclusion/exclusion criteria and begin treatment with the protocol assigned regimen. All evaluable patients are used in the analysis of safety, immune response, clinical response, OS and PFS.

Baseline Characteristics

Baseline characteristics on all evaluable patients are provided on demographic variables (age, sex, race/ethnicity), performance status, laboratory parameters, prior treatments, and disease characteristics, including tumor size, number of nodes involved, and metastatic sites.

Safety Profile

NCI CTCAE version 4.0 is used to evaluate the serious adverse events (SAEs) in each cycle of the treatment, and for 30 days beyond the last protocol specified treatment. Severity rates for each treatment arm are calculated and the corresponding exact 95% confidence interval (CI) are provided. All adverse events that are determined to be possibly, probably or definitely related to treatment are tabulated according to grade and type (according to the NCI CTCAE, Version 4.0). For each adverse event category, frequencies are tabulated by treatment group according to the highest grade per patient within 30 days after any study treatment.

Efficacy Analysis

The immune response rate, defined as proportion of patients that responded to 3 out of the 6 peptides, for each study arm is calculated with 95% exact CI. The clinical response rate for each study arm is estimated by the percent-

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age of patients achieving CR or PR by RECIST criteria, with corresponding exact 95% CI. Both immune response rate and clinical response rate of the two treatment groups are compared using Fisher exact test. The immune response for the B-raf mutant carrier and non-carrier in is also evaluated.

The Kaplan-Meier estimate of PFS and OS with corresponding 95% confidence band is provided for each dose level. The corresponding median survival time (with 95% confidence limits) is determined, along with OS and PFS estimates at selected time points. The exact log rank test is used to compare the PFS and OS between the two study arms.

The association between the positive immune response and:

- a. Objective clinical response.
- b. CD8+ T cell infiltration in tumor after cycle 1.
- c. Reduction in suppressor cells in the tumor and blood.
- d. Reduction in blood vessel density in the tumor after cycle 1.
- e. Reduction in EphA2 protein expression in tumor after cycle 1.
- f. Increased level of the CXCR3 ligand chemokine CXCL10/IP-10 in patient serum after cycle 1 is evaluated.

Chi-square (or Fisher exact) test is used to test the association between immune response and the categorical outcomes (e.g. objective clinical response). Wilcoxon test is used to compare the continuous outcomes (e.g. CD8+ T cell infiltration, suppressor cell populations, tumor blood vessel density, EphA2 protein expression, chemokine level) between the immune responders and non-responders.

It will be apparent that the precise details of the methods or compositions described may be varied or modified without departing from the spirit of the described invention. We claim all such modifications and variations fall within the scope and spirit of the claims below.

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130         135         140

Val  Asp  Asp  Glu  Gly  Arg  Ala  Ser  His  Ala  Ser  Cys  Leu  Cys  Pro  Pro
145         150         155         160

Gly  Phe  Ser  Gly  Asn  Phe  Cys  Glu  Ile  Val  Ala  Asn  Ser  Cys  Thr  Pro
165         170         175

Asn  Pro  Cys  Glu  Asn  Asp  Gly  Val  Cys  Thr  Asp  Ile  Gly  Gly  Asp  Phe
180         185         190

Arg  Cys  Arg  Cys  Pro  Ala  Gly  Phe  Ile  Asp  Lys  Thr  Cys  Ser  Arg  Pro
195         200         205

Val  Thr  Asn  Cys  Ala  Ser  Ser  Pro  Cys  Gln  Asn  Gly  Gly  Thr  Cys  Leu
210         215         220

Gln  His  Thr  Gln  Val  Ser  Tyr  Glu  Cys  Leu  Cys  Lys  Pro  Glu  Phe  Thr
225         230         235         240

Gly  Leu  Thr  Cys  Val  Lys  Lys  Arg  Ala  Leu  Ser  Pro  Gln  Gln  Val  Thr
245         250         255

Arg  Leu  Pro  Ser  Gly  Tyr  Gly  Leu  Ala  Tyr  Arg  Leu  Thr  Pro  Gly  Val
260         265         270

His  Glu  Leu  Pro  Val  Gln  Gln  Pro  Glu  His  Arg  Ile  Leu  Lys  Val  Ser
275         280         285

Met  Lys  Glu  Leu  Asn  Lys  Lys  Thr  Pro  Leu  Leu  Thr  Glu  Gly  Gln  Ala
290         295         300

Ile  Cys  Phe  Thr  Ile  Leu  Gly  Val  Leu  Thr  Ser  Leu  Val  Val  Leu  Gly
305         310         315         320

Thr  Val  Gly  Ile  Val  Phe  Leu  Asn  Lys  Cys  Glu  Thr  Trp  Val  Ser  Asn
325         330         335

Leu  Arg  Tyr  Asn  His  Met  Leu  Arg  Lys  Lys  Lys  Asn  Leu  Leu  Leu  Gln
340         345         350

Tyr  Asn  Ser  Gly  Glu  Asp  Leu  Ala  Val  Asn  Ile  Ile  Phe  Pro  Glu  Lys
355         360         365

Ile  Asp  Met  Thr  Thr  Phe  Ser  Lys  Glu  Ala  Gly  Asp  Glu  Glu  Ile
370         375         380

<210> SEQ ID NO 22
<211> LENGTH: 147
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

Met  Val  His  Leu  Thr  Pro  Glu  Glu  Lys  Ser  Ala  Val  Thr  Ala  Leu  Trp
1          5          10         15

Gly  Lys  Val  Asn  Val  Asp  Glu  Val  Gly  Gly  Glu  Ala  Leu  Gly  Arg  Leu
20         25         30

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[illegible]

```
<210> SEQ ID NO 23
<211> LENGTH: 923
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
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<400> SEQUENCE: 23

Met 1	Glu	Arg	Gly	Leu 5	Pro	Leu	Leu	Cys	Ala	Val	Leu	Ala	Leu	Val	Leu
Ala	Pro	Ala	Gly 20	Ala	Phe	Arg	Asn	Asp 25	Lys	Cys	Gly	Asp 30	Thr	Ile	Lys
Ile	Glu	Ser 35	Pro	Gly	Tyr	Leu	Thr 40	Ser	Pro	Gly	Tyr 45	Pro	His	Ser	Tyr
His 50	Pro	Ser	Glu	Lys	Cys	Glu 55	Trp	Leu	Ile	Gln	Ala 60	Pro	Asp	Pro	Tyr
Gln 65	Arg	Ile	Met	Ile	Asn 70	Phe	Asn	Pro	His	Phe 75	Asp	Leu	Glu	Asp	Arg 80
Asp	Cys	Lys	Tyr 85	Asp	Tyr	Val	Glu	Val	Phe 90	Asp	Gly	Glu	Asn	Glu	Asn 95
Gly	His	Phe	Arg 100	Gly	Lys	Phe	Cys	Gly 105	Lys	Ile	Ala	Pro	Pro	Pro	Val
Val	Ser	Ser	Gly 115	Pro	Phe	Leu	Phe 120	Ile	Lys	Phe	Val	Ser 125	Asp	Tyr	Glu
Thr 130	His	Gly	Ala	Gly	Phe 135	Ser	Ile	Arg	Tyr	Glu	Ile 140	Phe	Lys	Arg	Gly
Pro 145	Glu	Cys	Ser	Gln 150	Asn	Tyr	Thr	Thr	Pro	Ser 155	Gly	Val	Ile	Lys	Ser 160
Pro	Gly	Phe	Pro	Glu 165	Lys	Tyr	Pro	Asn	Ser 170	Leu	Glu	Cys	Thr	Tyr	Ile 175
Val	Phe	Val	Pro 180	Lys	Met	Ser	Glu	Ile 185	Ile	Leu	Glu	Phe	Glu	Ser	Phe 190
Asp	Leu	Glu	Pro 195	Asp	Ser	Asn	Pro 200	Pro	Gly	Gly	Met 205	Phe	Cys	Arg	Tyr
Asp 210	Arg	Leu	Glu	Ile	Trp 215	Asp	Gly	Phe	Pro	Asp 220	Val	Gly	Pro	His	Ile
Gly 225	Arg	Tyr	Cys	Gly 230	Gln	Lys	Thr	Pro	Gly	Arg 235	Ile	Arg	Ser	Ser	Ser 240
Gly	Ile	Leu	Ser 245	Met	Val	Phe	Tyr	Thr	Asp 250	Ser	Ala	Ile	Ala	Lys 255	Glu

Gly 260	Phe	Ser	Ala	Asn	Tyr	Ser	Val	Leu	Gln	Ser	Ser	Val	Ser	Glu	Asp
Phe 275	Lys	Cys	Met	Glu	Ala	Leu	Gly	Met	Glu	Ser	Gly	Glu	Ile	His	Ser
Asp 290	Gln	Ile	Thr	Ala	Ser	Ser	Gln	Tyr	Ser	Thr	Asn	Trp	Ser	Ala	Glu
Arg 305	Ser	Arg	Leu	Asn	Tyr	Pro	Glu	Asn	Gly	Trp	Thr	Pro	Gly	Glu	Asp
Ser	Tyr	Arg	Glu	Trp	Ile	Gln	Val	Asp	Leu	Gly	Leu	Leu	Arg	Phe	Val
Thr	Ala	Val	Gly	Thr	Gln	Gly	Ala	Ile	Ser	Lys	Glu	Thr	Lys	Lys	Lys
Tyr	Tyr	Val	Lys	Thr	Tyr	Lys	Ile	Asp	Val	Ser	Ser	Asn	Gly	Glu	Asp
Trp	Ile	Thr	Ile	Lys	Glu	Gly	Asn	Lys	Pro	Val	Leu	Phe	Gln	Gly	Asn
Thr 385	Asn	Pro	Thr	Asp	Val	Val	Val	Ala	Val	Phe	Pro	Lys	Pro	Leu	Ile
Thr	Arg	Phe	Val	Arg	Ile	Lys	Pro	Ala	Thr	Trp	Glu	Thr	Gly	Ile	Ser
Met	Arg	Phe	Glu	Val	Tyr	Gly	Cys	Lys	Ile	Thr	Asp	Tyr	Pro	Cys	Ser
Gly	Met	Leu	Gly	Met	Val	Ser	Gly	Leu	Ile	Ser	Asp	Ser	Gln	Ile	Thr
Ser	Ser	Asn	Gln	Gly	Asp	Arg	Asn	Trp	Met	Pro	Glu	Asn	Ile	Arg	Leu
Val 465	Thr	Ser	Arg	Ser	Gly	Trp	Ala	Leu	Pro	Pro	Ala	Pro	His	Ser	Tyr
Ile	Asn	Glu	Trp	Leu	Gln	Ile	Asp	Leu	Gly	Glu	Glu	Lys	Ile	Val	Arg
Gly	Ile	Ile	Ile	Gln	Gly	Gly	Lys	His	Arg	Glu	Asn	Lys	Val	Phe	Met
Arg	Lys	Phe	Lys	Ile	Gly	Tyr	Ser	Asn	Asn	Gly	Ser	Asp	Trp	Lys	Met
Ile	Met	Asp	Asp	Ser	Lys	Arg	Lys	Ala	Lys	Ser	Phe	Glu	Gly	Asn	Asn
Asn 545	Tyr	Asp	Thr	Pro	Glu	Leu	Arg	Thr	Phe	Pro	Ala	Leu	Ser	Thr	Arg
Phe	Ile	Arg	Ile	Tyr	Pro	Glu	Arg	Ala	Thr	His	Gly	Gly	Leu	Gly	Leu
Arg	Met	Glu	Leu	Leu	Gly	Cys	Glu	Val	Glu	Ala	Pro	Thr	Ala	Gly	Pro
Thr	Thr	Pro	Asn	Gly	Asn	Leu	Val	Asp	Glu	Cys	Asp	Asp	Asp	Gln	Ala
Asn 610	Cys	His	Ser	Gly	Thr	Gly	Asp	Asp	Phe	Gln	Leu	Thr	Gly	Gly	Thr
Thr 625	Val	Leu	Ala	Thr	Glu	Lys	Pro	Thr	Val	Ile	Asp	Ser	Thr	Ile	Gln
Ser	Glu	Phe	Pro	Thr	Tyr	Gly	Phe	Asn	Cys	Glu	Phe	Gly	Trp	Gly	Ser
His	Lys	Thr	Phe	Cys	His	Trp	Glu	His	Asp	Asn	His	Val	Gln	Leu	Lys

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Trp Ser Val Leu Thr Ser Lys Thr Gly Pro Ile Gln Asp His Thr Gly
 675 680 685
 Asp Gly Asn Phe Ile Tyr Ser Gln Ala Asp Glu Asn Gln Lys Gly Lys
 690 695 700
 Val Ala Arg Leu Val Ser Pro Val Val Tyr Ser Gln Asn Ser Ala His
 705 710 715 720
 Cys Met Thr Phe Trp Tyr His Met Ser Gly Ser His Val Gly Thr Leu
 725 730 735
 Arg Val Lys Leu Arg Tyr Gln Lys Pro Glu Glu Tyr Asp Gln Leu Val
 740 745 750
 Trp Met Ala Ile Gly His Gln Gly Asp His Trp Lys Glu Gly Arg Val
 755 760 765
 Leu Leu His Lys Ser Leu Lys Leu Tyr Gln Val Ile Phe Glu Gly Glu
 770 775 780
 Ile Gly Lys Gly Asn Leu Gly Gly Ile Ala Val Asp Asp Ile Ser Ile
 785 790 795 800
 Asn Asn His Ile Ser Gln Glu Asp Cys Ala Lys Pro Ala Asp Leu Asp
 805 810 815
 Lys Lys Asn Pro Glu Ile Lys Ile Asp Glu Thr Gly Ser Thr Pro Gly
 820 825 830
 Tyr Glu Gly Glu Gly Glu Gly Asp Lys Asn Ile Ser Arg Lys Pro Gly
 835 840 845
 Asn Val Leu Lys Thr Leu Asp Pro Ile Leu Ile Thr Ile Ile Ala Met
 850 855 860
 Ser Ala Leu Gly Val Leu Leu Gly Ala Val Cys Gly Val Val Leu Tyr
 865 870 875 880
 Cys Ala Cys Trp His Asn Gly Met Ser Glu Arg Asn Leu Ser Ala Leu
 885 890 895
 Glu Asn Tyr Asn Phe Glu Leu Val Asp Gly Val Lys Leu Lys Lys Asp
 900 905 910
 Lys Leu Asn Thr Gln Ser Thr Tyr Ser Glu Ala
 915 920

<210> SEQ ID NO 24

<211> LENGTH: 757

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 24

Met Leu Leu Arg Leu Leu Leu Ala Trp Ala Ala Ala Gly Pro Thr Leu
 1 5 10 15
 Gly Gln Asp Pro Trp Ala Ala Glu Pro Arg Ala Ala Cys Gly Pro Ser
 20 25 30
 Ser Cys Tyr Ala Leu Phe Pro Arg Arg Arg Thr Phe Leu Glu Ala Trp
 35 40 45
 Arg Ala Cys Arg Glu Leu Gly Gly Asp Leu Ala Thr Pro Arg Thr Pro
 50 55 60
 Glu Glu Ala Gln Arg Val Asp Ser Leu Val Gly Ala Gly Pro Ala Ser
 65 70 75 80
 Arg Leu Leu Trp Ile Gly Leu Gln Arg Gln Ala Arg Gln Cys Gln Leu
 85 90 95
 Gln Arg Pro Leu Arg Gly Phe Thr Trp Thr Thr Gly Asp Gln Asp Thr
 100 105 110
 Ala Phe Thr Asn Trp Ala Gln Pro Ala Ser Gly Gly Pro Cys Pro Ala
 115 120 125

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Gln	Arg	Cys	Val	Ala	Leu	Glu	Ala	Ser	Gly	Glu	His	Arg	Trp	Leu	Glu
130						135					140				
Gly	Ser	Cys	Thr	Leu	Ala	Val	Asp	Gly	Tyr	Leu	Cys	Gln	Phe	Gly	Phe
145				150						155					160
Glu	Gly	Ala	Cys	Pro	Ala	Leu	Gln	Asp	Glu	Ala	Gly	Gln	Ala	Gly	Pro
				165					170						175
Ala	Val	Tyr	Thr	Thr	Pro	Phe	His	Leu	Val	Ser	Thr	Glu	Phe	Glu	Trp
			180					185						190	
Leu	Pro	Phe	Gly	Ser	Val	Ala	Ala	Val	Gln	Cys	Gln	Ala	Gly	Arg	Gly
		195				200						205			
Ala	Ser	Leu	Leu	Cys	Val	Lys	Gln	Pro	Glu	Gly	Gly	Val	Gly	Trp	Ser
		210				215					220				
Arg	Ala	Gly	Pro	Leu	Cys	Leu	Gly	Thr	Gly	Cys	Ser	Pro	Asp	Asn	Gly
225					230					235					240
Gly	Cys	Glu	His	Glu	Cys	Val	Glu	Glu	Val	Asp	Gly	His	Val	Ser	Cys
				245					250					255	
Arg	Cys	Thr	Glu	Gly	Phe	Arg	Leu	Ala	Ala	Asp	Gly	Arg	Ser	Cys	Glu
			260					265						270	
Asp	Pro	Cys	Ala	Gln	Ala	Pro	Cys	Glu	Gln	Gln	Cys	Glu	Pro	Gly	Gly
		275				280						285			
Pro	Gln	Gly	Tyr	Ser	Cys	His	Cys	Arg	Leu	Gly	Phe	Arg	Pro	Ala	Glu
		290				295					300				
Asp	Asp	Pro	His	Arg	Cys	Val	Asp	Thr	Asp	Glu	Cys	Gln	Ile	Ala	Gly
305					310					315					320
Val	Cys	Gln	Gln	Met	Cys	Val	Asn	Tyr	Val	Gly	Gly	Phe	Glu	Cys	Tyr
				325					330					335	
Cys	Ser	Glu	Gly	His	Glu	Leu	Glu	Ala	Asp	Gly	Ile	Ser	Cys	Ser	Pro
			340					345					350		
Ala	Gly	Ala	Met	Gly	Ala	Gln	Ala	Ser	Gln	Asp	Leu	Gly	Asp	Glu	Leu
			355				360					365			
Leu	Asp	Asp	Gly	Glu	Asp	Glu	Glu	Asp	Glu	Asp	Glu	Ala	Trp	Lys	Ala
	370					375					380				
Phe	Asn	Gly	Gly	Trp	Thr	Glu	Met	Pro	Gly	Ile	Leu	Trp	Met	Glu	Pro
385					390					395					400
Thr	Gln	Pro	Pro	Asp	Phe	Ala	Leu	Ala	Tyr	Arg	Pro	Ser	Phe	Pro	Glu
				405					410					415	
Asp	Arg	Glu	Pro	Gln	Ile	Pro	Tyr	Pro	Glu	Pro	Thr	Trp	Pro	Pro	Pro
			420					425					430		
Leu	Ser	Ala	Pro	Arg	Val	Pro	Tyr	His	Ser	Ser	Val	Leu	Ser	Val	Thr
		435					440					445			
Arg	Pro	Val	Val	Val	Ser	Ala	Thr	His	Pro	Thr	Leu	Pro	Ser	Ala	His
		450				455					460				
Gln	Pro	Pro	Val	Ile	Pro	Ala	Thr	His	Pro	Ala	Leu	Ser	Arg	Asp	His
465					470					475					480
Gln	Ile	Pro	Val	Ile	Ala	Ala	Asn	Tyr	Pro	Asp	Leu	Pro	Ser	Ala	Tyr
				485					490					495	
Gln	Pro	Gly	Ile	Leu	Ser	Val	Ser	His	Ser	Ala	Gln	Pro	Pro	Ala	His
			500					505					510		
Gln	Pro	Pro	Met	Ile	Ser	Thr	Lys	Tyr	Pro	Glu	Leu	Phe	Pro	Ala	His
			515				520					525			
Gln	Ser	Pro	Met	Phe	Pro	Asp	Thr	Arg	Val	Ala	Gly	Thr	Gln	Thr	Thr
	530					535					540				

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Thr His Leu Pro Gly Ile Pro Pro Asn His Ala Pro Leu Val Thr Thr
 545 550 555 560
 Leu Gly Ala Gln Leu Pro Pro Gln Ala Pro Asp Ala Leu Val Leu Arg
 565 570 575
 Thr Gln Ala Thr Gln Leu Pro Ile Ile Pro Thr Ala Gln Pro Ser Leu
 580 585 590
 Thr Thr Thr Ser Arg Ser Pro Val Ser Pro Ala His Gln Ile Ser Val
 595 600 605
 Pro Ala Ala Thr Gln Pro Ala Ala Leu Pro Thr Leu Leu Pro Ser Gln
 610 615 620
 Ser Pro Thr Asn Gln Thr Ser Pro Ile Ser Pro Thr His Pro His Ser
 625 630 635 640
 Lys Ala Pro Gln Ile Pro Arg Glu Asp Gly Pro Ser Pro Lys Leu Ala
 645 650 655
 Leu Trp Leu Pro Ser Pro Ala Pro Thr Ala Ala Pro Thr Ala Leu Gly
 660 665 670
 Glu Ala Gly Leu Ala Glu His Ser Gln Arg Asp Asp Arg Trp Leu Leu
 675 680 685
 Val Ala Leu Leu Val Pro Thr Cys Val Phe Leu Val Val Leu Leu Ala
 690 695 700
 Leu Gly Ile Val Tyr Cys Thr Arg Cys Gly Pro His Ala Pro Asn Lys
 705 710 715 720
 Arg Ile Thr Asp Cys Tyr Arg Trp Val Ile His Ala Gly Ser Lys Ser
 725 730 735
 Pro Thr Glu Pro Met Pro Pro Arg Gly Ser Leu Thr Gly Val Gln Thr
 740 745 750
 Cys Arg Thr Ser Val
 755

<210> SEQ ID NO 25

<211> LENGTH: 976

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 25

Met Glu Leu Gln Ala Ala Arg Ala Cys Phe Ala Leu Leu Trp Gly Cys
 1 5 10 15
 Ala Leu Ala Ala Ala Ala Ala Ala Gln Gly Lys Glu Val Val Leu Leu
 20 25 30
 Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr
 35 40 45
 Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile
 50 55 60
 Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp
 65 70 75 80
 Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile
 85 90 95
 Glu Leu Lys Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala
 100 105 110
 Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu
 115 120 125
 Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr
 130 135 140
 Ile Ala Pro Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His
 145 150 155 160

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Val	Lys	Leu	Asn	Val	Glu	Glu	Arg	Ser	Val	Gly	Pro	Leu	Thr	Arg	Lys	
			165						170					175		
Gly	Phe	Tyr	Leu	Ala	Phe	Gln	Asp	Ile	Gly	Ala	Cys	Val	Ala	Leu	Leu	
			180					185					190			
Ser	Val	Arg	Val	Tyr	Tyr	Lys	Lys	Cys	Pro	Glu	Leu	Leu	Gln	Gly	Leu	
		195					200					205				
Ala	His	Phe	Pro	Glu	Thr	Ile	Ala	Gly	Ser	Asp	Ala	Pro	Ser	Leu	Ala	
	210					215				220						
Thr	Val	Ala	Gly	Thr	Cys	Val	Asp	His	Ala	Val	Val	Pro	Pro	Gly	Gly	
225					230					235					240	
Glu	Glu	Pro	Arg	Met	His	Cys	Ala	Val	Asp	Gly	Glu	Trp	Leu	Val	Pro	
			245						250				255			
Ile	Gly	Gln	Cys	Leu	Cys	Gln	Ala	Gly	Tyr	Glu	Lys	Val	Glu	Asp	Ala	
		260						265					270			
Cys	Gln	Ala	Cys	Ser	Pro	Gly	Phe	Phe	Lys	Phe	Glu	Ala	Ser	Glu	Ser	
	275						280					285				
Pro	Cys	Leu	Glu	Cys	Pro	Glu	His	Thr	Leu	Pro	Ser	Pro	Glu	Gly	Ala	
	290					295				300						
Thr	Ser	Cys	Glu	Cys	Glu	Glu	Gly	Phe	Phe	Arg	Ala	Pro	Gln	Asp	Pro	
305					310					315					320	
Ala	Ser	Met	Pro	Cys	Thr	Arg	Pro	Pro	Ser	Ala	Pro	His	Tyr	Leu	Thr	
			325					330					335			
Ala	Val	Gly	Met	Gly	Ala	Lys	Val	Glu	Leu	Arg	Trp	Thr	Pro	Pro	Gln	
		340						345					350			
Asp	Ser	Gly	Gly	Arg	Glu	Asp	Ile	Val	Tyr	Ser	Val	Thr	Cys	Glu	Gln	
	355					360						365				
Cys	Trp	Pro	Glu	Ser	Gly	Glu	Cys	Gly	Pro	Cys	Glu	Ala	Ser	Val	Arg	
	370					375					380					
Tyr	Ser	Glu	Pro	Pro	His	Gly	Leu	Thr	Arg	Thr	Ser	Val	Thr	Val	Ser	
385					390					395					400	
Asp	Leu	Glu	Pro	His	Met	Asn	Tyr	Thr	Phe	Thr	Val	Glu	Ala	Arg	Asn	
			405					410						415		
Gly	Val	Ser	Gly	Leu	Val	Thr	Ser	Arg	Ser	Phe	Arg	Thr	Ala	Ser	Val	
		420						425					430			
Ser	Ile	Asn	Gln	Thr	Glu	Pro	Pro	Lys	Val	Arg	Leu	Glu	Gly	Arg	Ser	
	435					440					445					
Thr	Thr	Ser	Leu	Ser	Val	Ser	Trp	Ser	Ile	Pro	Pro	Pro	Gln	Gln	Ser	
	450					455				460						
Arg	Val	Trp	Lys	Tyr	Glu	Val	Thr	Tyr	Arg	Lys	Lys	Gly	Asp	Ser	Asn	
465					470					475					480	
Ser	Tyr	Asn	Val	Arg	Arg	Thr	Glu	Gly	Phe	Ser	Val	Thr	Leu	Asp	Asp	
		485							490					495		
Leu	Ala	Pro	Asp	Thr	Thr	Tyr	Leu	Val	Gln	Val	Gln	Ala	Leu	Thr	Gln	
		500						505					510			
Glu	Gly	Gln	Gly	Ala	Gly	Ser	Lys	Val	His	Glu	Phe	Gln	Thr	Leu	Ser	
	515						520					525				
Pro	Glu	Gly	Ser	Gly	Asn	Leu	Ala	Val	Ile	Gly	Gly	Val	Ala	Val	Gly	
	530				535						540					
Val	Val	Leu	Leu	Leu	Val	Leu	Ala	Gly	Val	Gly	Phe	Phe	Ile	His	Arg	
545					550					555					560	
Arg	Arg	Lys	Asn	Gln	Arg	Ala	Arg	Gln	Ser	Pro	Glu	Asp	Val	Tyr	Phe	
			565					570						575		

Ser	Lys	Ser	Glu	Gln	Leu	Lys	Pro	Leu	Lys	Thr	Tyr	Val	Asp	Pro	His
			580					585					590		
Thr	Tyr	Glu	Asp	Pro	Asn	Gln	Ala	Val	Leu	Lys	Phe	Thr	Thr	Glu	Ile
		595					600					605			
His	Pro	Ser	Cys	Val	Thr	Arg	Gln	Lys	Val	Ile	Gly	Ala	Gly	Glu	Phe
						615					620				
Gly	Glu	Val	Tyr	Lys	Gly	Met	Leu	Lys	Thr	Ser	Ser	Gly	Lys	Lys	Glu
					630					635					640
Val	Pro	Val	Ala	Ile	Lys	Thr	Leu	Lys	Ala	Gly	Tyr	Thr	Glu	Lys	Gln
				645					650					655	
Arg	Val	Asp	Phe	Leu	Gly	Glu	Ala	Gly	Ile	Met	Gly	Gln	Phe	Ser	His
			660					665					670		
His	Asn	Ile	Ile	Arg	Leu	Glu	Gly	Val	Ile	Ser	Lys	Tyr	Lys	Pro	Met
			675				680					685			
Met	Ile	Ile	Thr	Glu	Tyr	Met	Glu	Asn	Gly	Ala	Leu	Asp	Lys	Phe	Leu
			690			695						700			
Arg	Glu	Lys	Asp	Gly	Glu	Phe	Ser	Val	Leu	Gln	Leu	Val	Gly	Met	Leu
					710					715					720
Arg	Gly	Ile	Ala	Ala	Gly	Met	Lys	Tyr	Leu	Ala	Asn	Met	Asn	Tyr	Val
				725					730					735	
His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Val	Asn	Ser	Asn	Leu	Val
			740					745					750		
Cys	Lys	Val	Ser	Asp	Phe	Gly	Leu	Ser	Arg	Val	Leu	Glu	Asp	Asp	Pro
			755				760					765			
Glu	Ala	Thr	Tyr	Thr	Thr	Ser	Gly	Gly	Lys	Ile	Pro	Ile	Arg	Trp	Thr
			770			775					780				
Ala	Pro	Glu	Ala	Ile	Ser	Tyr	Arg	Lys	Phe	Thr	Ser	Ala	Ser	Asp	Val
					790					795					800
Trp	Ser	Phe	Gly	Ile	Val	Met	Trp	Glu	Val	Met	Thr	Tyr	Gly	Glu	Arg
				805					810					815	
Pro	Tyr	Trp	Glu	Leu	Ser	Asn	His	Glu	Val	Met	Lys	Ala	Ile	Asn	Asp
			820					825					830		
Gly	Phe	Arg	Leu	Pro	Thr	Pro	Met	Asp	Cys	Pro	Ser	Ala	Ile	Tyr	Gln
			835				840					845			
Leu	Met	Met	Gln	Cys	Trp	Gln	Gln	Glu	Arg	Ala	Arg	Arg	Pro	Lys	Phe
			850			855					860				
Ala	Asp	Ile	Val	Ser	Ile	Leu	Asp	Lys	Leu	Ile	Arg	Ala	Pro	Asp	Ser
					870					875					880
Leu	Lys	Thr	Leu	Ala	Asp	Phe	Asp	Pro	Arg	Val	Ser	Ile	Arg	Leu	Pro
				885					890					895	
Ser	Thr	Ser	Gly	Ser	Glu	Gly	Val	Pro	Phe	Arg	Thr	Val	Ser	Glu	Trp
			900					905					910		
Leu	Glu	Ser	Ile	Lys	Met	Gln	Gln	Tyr	Thr	Glu	His	Phe	Met	Ala	Ala
			915				920					925			
Gly	Tyr	Thr	Ala	Ile	Glu	Lys	Val	Val	Gln	Met	Thr	Asn	Asp	Asp	Ile
			930			935					940				
Lys	Arg	Ile	Gly	Val</											

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<210> SEQ ID NO 26
<211> LENGTH: 181
<212> TYPE: PRT
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 26

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Met Cys Lys Gly Leu Ala Ala Leu Pro His Ser Cys Leu Glu Arg Ala
 1           5           10          15
Lys Glu Ile Lys Ile Lys Leu Gly Ile Leu Leu Gln Lys Pro Asp Ser
      20           25          30
Val Gly Asp Leu Val Ile Pro Tyr Asn Glu Lys Pro Glu Lys Pro Ala
      35           40          45
Lys Thr Gln Lys Thr Ser Leu Asp Glu Ala Leu Gln Trp Arg Asp Ser
      50           55          60
Leu Asp Lys Leu Leu Gln Asn Asn Tyr Gly Leu Ala Ser Phe Lys Ser
      65           70          75          80
Phe Leu Lys Ser Glu Phe Ser Glu Glu Asn Leu Glu Phe Trp Ile Ala
      85           90          95
Cys Glu Asp Tyr Lys Lys Ile Lys Ser Pro Ala Lys Met Ala Glu Lys
      100          105          110
Ala Lys Gln Ile Tyr Glu Glu Phe Ile Gln Thr Glu Ala Pro Lys Glu
      115          120          125
Val Asn Ile Asp His Phe Thr Lys Asp Ile Thr Met Lys Asn Leu Val
      130          135          140
Glu Pro Ser Leu Ser Ser Phe Asp Met Ala Gln Lys Arg Ile His Ala
      145          150          155          160
Leu Met Glu Lys Asp Ser Leu Pro Arg Phe Val Arg Ser Glu Phe Tyr
      165          170          175
Gln Glu Leu Ile Lys
      180

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<210> SEQ ID NO 27

<211> LENGTH: 1106

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 27

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Met Arg Leu Pro Gly Ala Met Pro Ala Leu Ala Leu Lys Gly Glu Leu
 1           5           10          15
Leu Leu Leu Ser Leu Leu Leu Leu Glu Pro Gln Ile Ser Gln Gly
      20           25          30
Leu Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn Val Ser Ser
      35           40          45
Thr Phe Val Leu Thr Cys Ser Gly Ser Ala Pro Val Val Trp Glu Arg
      50           55          60
Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys Ala Gln Asp Gly Thr
      65           70          75          80
Phe Ser Ser Val Leu Thr Leu Thr Asn Leu Thr Gly Leu Asp Thr Gly
      85           90          95
Glu Tyr Phe Cys Thr His Asn Asp Ser Arg Gly Leu Glu Thr Asp Glu
      100          105          110
Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro Thr Val Gly Phe Leu
      115          120          125
Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu Thr Glu Ile Thr Glu
      130          135          140
Ile Thr Ile Pro Cys Arg Val Thr Asp Pro Gln Leu Val Val Thr Leu
      145          150          155          160
His Glu Lys Lys Gly Asp Val Ala Leu Pro Val Pro Tyr Asp His Gln

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165								170				175				
Arg	Gly	Phe	Ser 180	Gly	Ile	Phe	Glu	Asp 185	Arg	Ser	Tyr	Ile	Cys 190	Lys	Thr	
Thr	Ile	Gly 195	Asp	Arg	Glu	Val	Asp 200	Ser	Asp	Ala	Tyr	Tyr 205	Val	Tyr	Arg	
Leu	Gln 210	Val	Ser	Ser	Ile	Asn 215	Val	Ser	Val	Asn	Ala 220	Val	Gln	Thr	Val	
Val	Arg	Gln	Gly	Glu	Asn 230	Ile	Thr	Leu	Met	Cys 235	Ile	Val	Ile	Gly	Asn 240	
Glu	Val	Val	Asn 245	Phe	Glu	Trp	Thr	Tyr	Pro 250	Arg	Lys	Glu	Ser	Gly 255	Arg	
Leu	Val	Glu	Pro 260	Val	Thr	Asp	Phe	Leu 265	Leu	Asp	Met	Pro	Tyr 270	His	Ile	
Arg	Ser	Ile 275	Leu	His	Ile	Pro	Ser 280	Ala	Glu	Leu	Glu	Asp 285	Ser	Gly	Thr	
Tyr	Thr 290	Cys	Asn	Val	Thr	Glu 295	Ser	Val	Asn	Asp	His 300	Gln	Asp	Glu	Lys	
Ala	Ile	Asn	Ile	Thr	Val 310	Val	Glu	Ser	Gly	Tyr 315	Val	Arg	Leu	Leu	Gly 320	
Glu	Val	Gly	Thr	Leu 325	Gln	Phe	Ala	Glu	Leu 330	His	Arg	Ser	Arg	Thr	Leu	
Gln	Val	Val	Phe 340	Glu	Ala	Tyr	Pro	Pro 345	Pro	Thr	Val	Leu	Trp 350	Phe	Lys	
Asp	Asn	Arg 355	Thr	Leu	Gly	Asp	Ser 360	Ser	Ala	Gly	Glu	Ile 365	Ala	Leu	Ser	
Thr	Arg 370	Asn	Val	Ser	Glu	Thr 375	Arg	Tyr	Val	Ser	Glu 380	Leu	Thr	Leu	Val	
Arg	Val	Lys	Val	Ala	Glu 390	Ala	Gly	His	Tyr	Thr 395	Met	Arg	Ala	Phe	His 400	
Glu	Asp	Ala	Glu	Val 405	Gln	Leu	Ser	Phe	Gln 410	Leu	Gln	Ile	Asn	Val	Pro 415	
Val	Arg	Val	Leu 420	Glu	Leu	Ser	Glu	Ser 425	His	Pro	Asp	Ser	Gly 430	Glu	Gln	
Thr	Val	Arg 435	Cys	Arg	Gly	Arg	Gly 440	Met	Pro	Gln	Pro	Asn 445	Ile	Ile	Trp	
Ser	Ala 450	Cys	Arg	Asp	Leu	Lys 455	Arg	Cys	Pro	Arg	Glu 460	Leu	Pro	Pro	Thr	
Leu	Leu	Gly	Asn	Ser	Ser 470	Glu	Glu	Glu	Ser	Gln 475	Leu	Glu	Thr	Asn	Val 480	
Thr	Tyr	Trp	Glu 485	Glu	Glu	Gln	Glu	Phe	Glu 490	Val	Val	Ser	Thr	Leu	Arg 495	
Leu	Gln	His	Val 500	Asp	Arg	Pro	Leu	Ser 505	Val	Arg	Cys	Thr	Leu 510	Arg	Asn	
Ala	Val	Gly 515	Gln	Asp	Thr	Gln	Glu 520	Val	Ile	Val	Val	Pro 525	His	Ser	Leu	
Pro	Phe 530	Lys	Val	Val	Val	Ile 535	Ser	Ala	Ile	Leu	Ala 540	Leu	Val	Val	Leu	
Thr	Ile	Ile	Ser	Leu	Ile 550	Ile	Leu	Ile	Met	Leu 555	Trp	Gln	Lys	Lys	Pro 560	
Arg	Tyr	Glu	Ile 565	Arg	Trp	Lys	Val	Ile	Glu 570	Ser	Val	Ser	Ser	Asp	Gly 575	
His	Glu	Tyr	Ile 580	Tyr	Val	Asp	Pro	Met 585	Gln	Leu	Pro	Tyr	Asp 590	Ser	Thr	

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Trp Glu Leu Pro Arg Asp Gln Leu Val Leu Gly Arg Thr Leu Gly Ser
 595 600 605
 Gly Ala Phe Gly Gln Val Val Glu Ala Thr Ala His Gly Leu Ser His
 610 615 620
 Ser Gln Ala Thr Met Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala
 625 630 635 640
 Arg Ser Ser Glu Lys Gln Ala Leu Met Ser Glu Leu Lys Ile Met Ser
 645 650 655
 His Leu Gly Pro His Leu Asn Val Val Asn Leu Leu Gly Ala Cys Thr
 660 665 670
 Lys Gly Gly Pro Ile Tyr Ile Ile Thr Glu Tyr Cys Arg Tyr Gly Asp
 675 680 685
 Leu Val Asp Tyr Leu His Arg Asn Lys His Thr Phe Leu Gln His His
 690 695 700
 Ser Asp Lys Arg Arg Pro Pro Ser Ala Glu Leu Tyr Ser Asn Ala Leu
 705 710 715 720
 Pro Val Gly Leu Pro Leu Pro Ser His Val Ser Leu Thr Gly Glu Ser
 725 730 735
 Asp Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Val Asp Tyr Val
 740 745 750
 Pro Met Leu Asp Met Lys Gly Asp Val Lys Tyr Ala Asp Ile Glu Ser
 755 760 765
 Ser Asn Tyr Met Ala Pro Tyr Asp Asn Tyr Val Pro Ser Ala Pro Glu
 770 775 780
 Arg Thr Cys Arg Ala Thr Leu Ile Asn Glu Ser Pro Val Leu Ser Tyr
 785 790 795 800
 Met Asp Leu Val Gly Phe Ser Tyr Gln Val Ala Asn Gly Met Glu Phe
 805 810 815
 Leu Ala Ser Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg Asn Val
 820 825 830
 Leu Ile Cys Glu Gly Lys Leu Val Lys Ile Cys Asp Phe Gly Leu Ala
 835 840 845
 Arg Asp Ile Met Arg Asp Ser Asn Tyr Ile Ser Lys Gly Ser Thr Phe
 850 855 860
 Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Ser Leu Tyr
 865 870 875 880
 Thr Thr Leu Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile
 885 890 895
 Phe Thr Leu Gly Gly Thr Pro Tyr Pro Glu Leu Pro Met Asn Glu Gln
 900 905 910
 Phe Tyr Asn Ala Ile Lys Arg Gly Tyr Arg Met Ala Gln Pro Ala His
 915 920 925
 Ala Ser Asp Glu Ile Tyr Glu Ile Met Gln Lys Cys Trp Glu Glu Lys
 930 935 940
 Phe Glu Ile Arg Pro Pro Phe Ser Gln Leu Val Leu Leu Leu Glu Arg
 945 950 955 960
 Leu Leu Gly Glu Gly Tyr Lys Lys Lys Tyr Gln Gln Val Asp Glu Glu
 965 970 975
 Phe Leu Arg Ser Asp His Pro Ala Ile Leu Arg Ser Gln Ala Arg Leu
 980 985 990
 Pro Gly Phe His Gly Leu Arg Ser Pro Leu Asp Thr Ser Ser Val Leu
 995 1000 1005

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Tyr	Thr	Ala	Val	Gln	Pro	Asn	Glu	Gly	Asp	Asn	Asp	Tyr	Ile	Ile
1010						1015						1020		
Pro	Leu	Pro	Asp	Pro	Lys	Pro	Glu	Val	Ala	Asp	Glu	Gly	Pro	Leu
1025						1030					1035			
Glu	Gly	Ser	Pro	Ser	Leu	Ala	Ser	Ser	Thr	Leu	Asn	Glu	Val	Asn
1040						1045					1050			
Thr	Ser	Ser	Thr	Ile	Ser	Cys	Asp	Ser	Pro	Leu	Glu	Pro	Gln	Asp
1055						1060					1065			
Glu	Pro	Glu	Pro	Glu	Pro	Gln	Leu	Glu	Leu	Gln	Val	Glu	Pro	Glu
1070						1075					1080			
Pro	Glu	Leu	Glu	Gln	Leu	Pro	Asp	Ser	Gly	Cys	Pro	Ala	Pro	Arg
1085						1090					1095			
Ala	Glu	Ala	Glu	Asp	Ser	Phe	Leu							
1100						1105								

<210> SEQ ID NO 28

<211> LENGTH: 2322

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 28

Met	Gln	Ser	Gly	Arg	Gly	Pro	Pro	Leu	Pro	Ala	Pro	Gly	Leu	Ala	Leu
1				5					10					15	
Ala	Leu	Thr	Leu	Thr	Met	Leu	Ala	Arg	Leu	Ala	Ser	Ala	Ala	Ser	Phe
		20					25						30		
Phe	Gly	Glu	Asn	His	Leu	Glu	Val	Pro	Val	Ala	Thr	Ala	Leu	Thr	Asp
	35					40						45			
Ile	Asp	Leu	Gln	Leu	Gln	Phe	Ser	Thr	Ser	Gln	Pro	Glu	Ala	Leu	Leu
50					55						60				
Leu	Leu	Ala	Ala	Gly	Pro	Ala	Asp	His	Leu	Leu	Gln	Leu	Tyr	Ser	
65				70					75				80		
Gly	Arg	Leu	Gln	Val	Arg	Leu	Val	Leu	Gly	Gln	Glu	Glu	Leu	Arg	Leu
			85					90					95		
Gln	Thr	Pro	Ala	Glu	Thr	Leu	Leu	Ser	Asp	Ser	Ile	Pro	His	Thr	Val
		100						105					110		
Val	Leu	Thr	Val	Val	Glu	Gly	Trp	Ala	Thr	Leu	Ser	Val	Asp	Gly	Phe
	115					120						125			
Leu	Asn	Ala	Ser	Ser	Ala	Val	Pro	Gly	Ala	Pro	Leu	Glu	Val	Pro	Tyr
130					135						140				
Gly	Leu	Phe	Val	Gly	Gly	Thr	Gly	Thr	Leu	Gly	Leu	Pro	Tyr	Leu	Arg
145				150					155					160	
Gly	Thr	Ser	Arg	Pro	Leu	Arg	Gly	Cys	Leu	His	Ala	Ala	Thr	Leu	Asn
			165					170						175	
Gly	Arg	Ser	Leu	Leu	Arg	Pro	Leu	Thr	Pro	Asp	Val	His	Glu	Gly	Cys
		180						185					190		
Ala	Glu	Glu	Phe	Ser	Ala	Ser	Asp	Asp	Val	Ala	Leu	Gly	Phe	Ser	Gly
	195						200					205			
Pro	His	Ser	Leu	Ala	Ala	Phe	Pro	Ala	Trp	Gly	Thr	Gln	Asp	Glu	Gly
210					215						220				
Thr	Leu	Glu	Phe	Thr	Leu	Thr	Thr	Gln	Ser	Arg	Gln	Ala	Pro	Leu	Ala
225					230					235				240	
Phe	Gln	Ala	Gly	Gly	Arg	Arg	Gly	Asp	Phe	Ile	Tyr	Val	Asp	Ile	Phe
		245						250						255	
Glu	Gly	His	Leu	Arg	Ala	Val	Val	Glu	Lys	Gly	Gln	Gly	Thr	Val	Leu
		260						265					270		

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Leu	His	Asn	Ser	Val	Pro	Val	Ala	Asp	Gly	Gln	Pro	His	Glu	Val	Ser
	275						280					285			
Val	His	Ile	Asn	Ala	His	Arg	Leu	Glu	Ile	Ser	Val	Asp	Gln	Tyr	Pro
	290					295					300				
Thr	His	Thr	Ser	Asn	Arg	Gly	Val	Leu	Ser	Tyr	Leu	Glu	Pro	Arg	Gly
305					310					315					320
Ser	Leu	Leu	Leu	Gly	Gly	Leu	Asp	Ala	Glu	Ala	Ser	Arg	His	Leu	Gln
				325					330					335	
Glu	His	Arg	Leu	Gly	Leu	Thr	Pro	Glu	Ala	Thr	Asn	Ala	Ser	Leu	Leu
			340					345					350		
Gly	Cys	Met	Glu	Asp	Leu	Ser	Val	Asn	Gly	Gln	Arg	Arg	Gly	Leu	Arg
	355						360					365			
Glu	Ala	Leu	Leu	Thr	Arg	Asn	Met	Ala	Ala	Gly	Cys	Arg	Leu	Glu	Glu
	370					375					380				
Glu	Glu	Tyr	Glu	Asp	Asp	Ala	Tyr	Gly	His	Tyr	Glu	Ala	Phe	Ser	Thr
385					390					395					400
Leu	Ala	Pro	Glu	Ala	Trp	Pro	Ala	Met	Glu	Leu	Pro	Glu	Pro	Cys	Val
				405					410					415	
Pro	Glu	Pro	Gly	Leu	Pro	Pro	Val	Phe	Ala	Asn	Phe	Thr	Gln	Leu	Leu
			420					425					430		
Thr	Ile	Ser	Pro	Leu	Val	Val	Ala	Glu	Gly	Gly	Thr	Ala	Trp	Leu	Glu
	435						440					445			
Trp	Arg	His	Val	Gln	Pro	Thr	Leu	Asp	Leu	Met	Glu	Ala	Glu	Leu	Arg
450						455					460				
Lys	Ser	Gln	Val	Leu	Phe	Ser	Val	Thr	Arg	Gly	Ala	Arg	His	Gly	Glu
465					470					475					480
Leu	Glu	Leu	Asp	Ile	Pro	Gly	Ala	Gln	Ala	Arg	Lys	Met	Phe	Thr	Leu
			485						490					495	
Leu	Asp	Val	Val	Asn	Arg	Lys	Ala	Arg	Phe	Ile	His	Asp	Gly	Ser	Glu
		500						505					510		
Asp	Thr	Ser	Asp	Gln	Leu	Val	Leu	Glu	Val	Ser	Val	Thr	Ala	Arg	Val
	515						520					525			
Pro	Met	Pro	Ser	Cys	Leu	Arg	Arg	Gly	Gln	Thr	Tyr	Leu	Leu	Pro	Ile
	530					535					540				
Gln	Val	Asn	Pro	Val	Asn	Asp	Pro	Pro	His	Ile	Ile	Phe	Pro	His	Gly
545					550					555					560
Ser	Leu	Met	Val	Ile	Leu	Glu	His	Thr	Gln	Lys	Pro	Leu	Gly	Pro	Glu
				565					570					575	
Val	Phe	Gln	Ala	Tyr	Asp	Pro	Asp	Ser	Ala	Cys	Glu	Gly	Leu	Thr	Phe
		580						585					590		
Gln	Val	Leu	Gly	Thr	Ser	Ser	Gly	Leu	Pro	Val	Glu	Arg	Arg	Asp	Gln
	595						600				605				
Pro	Gly	Glu	Pro	Ala	Thr	Glu	Phe	Ser	Cys	Arg	Glu	Leu	Glu	Ala	Gly
	610					615					620				
Ser	Leu	Val	Tyr	Val	His	Arg	Gly	Gly	Pro	Ala	Gln	Asp	Leu	Thr	Phe
625					630					635					640
Arg	Val	Ser	Asp	Gly	Leu	Gln	Ala	Ser	Pro	Pro	Ala	Thr	Leu	Lys	Val
				645					650					655	
Val	Ala	Ile	Arg	Pro	Ala	Ile	Gln	Ile	His	Arg	Ser	Thr	Gly	Leu	Arg
		660					665						670		
Leu	Ala	Gln	Gly	Ser	Ala	Met	Pro	Ile	Leu	Pro	Ala	Asn	Leu	Ser	Val
	675						680					685			

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Glu Thr Asn Ala Val Gly Gln Asp Val Ser Val Leu Phe Arg Val Thr	690	695	700
Gly Ala Leu Gln Phe Gly Glu Leu Gln Lys Gln Gly Ala Gly Gly Val	705	710	715
Glu Gly Ala Glu Trp Trp Ala Thr Gln Ala Phe His Gln Arg Asp Val	725	730	735
Glu Gln Gly Arg Val Arg Tyr Leu Ser Thr Asp Pro Gln His His Ala	740	745	750
Tyr Asp Thr Val Glu Asn Leu Ala Leu Glu Val Gln Val Gly Gln Glu	755	760	765
Ile Leu Ser Asn Leu Ser Phe Pro Val Thr Ile Gln Arg Ala Thr Val	770	775	780
Trp Met Leu Arg Leu Glu Pro Leu His Thr Gln Asn Thr Gln Gln Glu	785	790	795
Thr Leu Thr Thr Ala His Leu Glu Ala Thr Leu Glu Glu Ala Gly Pro	805	810	815
Ser Pro Pro Thr Phe His Tyr Glu Val Val Gln Ala Pro Arg Lys Gly	820	825	830
Asn Leu Gln Leu Gln Gly Thr Arg Leu Ser Asp Gly Gln Gly Phe Thr	835	840	845
Gln Asp Asp Ile Gln Ala Gly Arg Val Thr Tyr Gly Ala Thr Ala Arg	850	855	860
Ala Ser Glu Ala Val Glu Asp Thr Phe Arg Phe Arg Val Thr Ala Pro	865	870	875
Pro Tyr Phe Ser Pro Leu Tyr Thr Phe Pro Ile His Ile Gly Gly Asp	885	890	895
Pro Asp Ala Pro Val Leu Thr Asn Val Leu Leu Val Val Pro Glu Gly	900	905	910
Gly Glu Gly Val Leu Ser Ala Asp His Leu Phe Val Lys Ser Leu Asn	915	920	925
Ser Ala Ser Tyr Leu Tyr Glu Val Met Glu Arg Pro Arg His Gly Arg	930	935	940
Leu Ala Trp Arg Gly Thr Gln Asp Lys Thr Thr Met Val Thr Ser Phe	945	950	955
Thr Asn Glu Asp Leu Leu Arg Gly Arg Leu Val Tyr Gln His Asp Asp	965	970	975
Ser Glu Thr Thr Glu Asp Asp Ile Pro Phe Val Ala Thr Arg Gln Gly	980	985	990
Glu Ser Ser Gly Asp Met Ala Trp Glu Glu Val Arg Gly Val Phe Arg	995	1000	1005
Val Ala Ile Gln Pro Val Asn Asp His Ala Pro Val Gln Thr Ile	1010	1015	1020
Ser Arg Ile Phe His Val Ala Arg Gly Gly Arg Arg Leu Leu Thr	1025	1030	1035
Thr Asp Asp Val Ala Phe Ser Asp Ala Asp Ser Gly Phe Ala Asp	1040	1045	1050
Ala Gln Leu Val Leu Thr Arg Lys Asp Leu Leu Phe Gly Ser Ile	1055	1060	1065
Val Ala Val Asp Glu Pro Thr Arg Pro Ile Tyr Arg Phe Thr Gln	1070	1075	1080
Glu Asp Leu Arg Lys Arg Arg Val Leu Phe Val His Ser Gly Ala	1085	1090	1095
Asp Arg Gly Trp Ile Gln Leu Gln Val Ser Asp Gly Gln His Gln			

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1100	1105	1110
Ala Thr Ala Leu Leu Glu Val	Gln Ala Ser Glu Pro	Tyr Leu Arg
1115	1120	1125
Val Ala Asn Gly Ser Ser Leu	Val Val Pro Gln Gly	Gly Gln Gly
1130	1135	1140
Thr Ile Asp Thr Ala Val Leu	His Leu Asp Thr Asn	Leu Asp Ile
1145	1150	1155
Arg Ser Gly Asp Glu Val His	Tyr His Val Thr Ala	Gly Pro Arg
1160	1165	1170
Trp Gly Gln Leu Val Arg Ala	Gly Gln Pro Ala Thr	Ala Phe Ser
1175	1180	1185
Gln Gln Asp Leu Leu Asp Gly	Ala Val Leu Tyr Ser	His Asn Gly
1190	1195	1200
Ser Leu Ser Pro Arg Asp Thr	Met Ala Phe Ser Val	Glu Ala Gly
1205	1210	1215
Pro Val His Thr Asp Ala Thr	Leu Gln Val Thr Ile	Ala Leu Glu
1220	1225	1230
Gly Pro Leu Ala Pro Leu Lys	Leu Val Arg His Lys	Lys Ile Tyr
1235	1240	1245
Val Phe Gln Gly Glu Ala Ala	Glu Ile Arg Arg Asp	Gln Leu Glu
1250	1255	1260
Ala Ala Gln Glu Ala Val Pro	Pro Ala Asp Ile Val	Phe Ser Val
1265	1270	1275
Lys Ser Pro Pro Ser Ala Gly	Tyr Leu Val Met Val	Ser Arg Gly
1280	1285	1290
Ala Leu Ala Asp Glu Pro Pro	Ser Leu Asp Pro Val	Gln Ser Phe
1295	1300	1305
Ser Gln Glu Ala Val Asp Thr	Gly Arg Val Leu Tyr	Leu His Ser
1310	1315	1320
Arg Pro Glu Ala Trp Ser Asp	Ala Phe Ser Leu Asp	Val Ala Ser
1325	1330	1335
Gly Leu Gly Ala Pro Leu Glu	Gly Val Leu Val Glu	Leu Glu Val
1340	1345	1350
Leu Pro Ala Ala Ile Pro Leu	Glu Ala Gln Asn Phe	Ser Val Pro
1355	1360	1365
Glu Gly Gly Ser Leu Thr Leu	Ala Pro Pro Leu Leu	Arg Val Ser
1370	1375	1380
Gly Pro Tyr Phe Pro Thr Leu	Leu Gly Leu Ser Leu	Gln Val Leu
1385	1390	1395
Glu Pro Pro Gln His Gly Ala	Leu Gln Lys Glu Asp	Gly Pro Gln
1400	1405	1410
Ala Arg Thr Leu Ser Ala Phe	Ser Trp Arg Met Val	Glu Glu Gln
1415	1420	1425
Leu Ile Arg Tyr Val His Asp	Gly Ser Glu Thr Leu	Thr Asp Ser
1430	1435	1440
Phe Val Leu Met Ala Asn Ala	Ser Glu Met Asp Arg	Gln Ser His
1445	1450	1455
Pro Val Ala Phe Thr Val Thr	Val Leu Pro Val Asn	Asp Gln Pro
1460	1465	1470
Pro Ile Leu Thr Thr Asn Thr	Gly Leu Gln Met Trp	Glu Gly Ala
1475	1480	1485
Thr Ala Pro Ile Pro Ala Glu	Ala Leu Arg Ser Thr	Asp Gly Asp
1490	1495	1500

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Ser Gly 1505	Ser Glu Asp Leu Val 1510	Tyr Thr Ile Glu Gln 1515	Pro Ser Asn
Gly Arg 1520	Val Val Leu Arg Gly 1525	Ala Pro Gly Thr Glu 1530	Val Arg Ser
Phe Thr 1535	Gln Ala Gln Leu Asp 1540	Gly Gly Leu Val Leu 1545	Phe Ser His
Arg Gly 1550	Thr Leu Asp Gly Gly 1555	Phe Arg Phe Arg Leu 1560	Ser Asp Gly
Glu His 1565	Thr Ser Pro Gly His 1570	Phe Phe Arg Val Thr 1575	Ala Gln Lys
Gln Val 1580	Leu Leu Ser Leu Lys 1585	Gly Ser Gln Thr Leu 1590	Thr Val Cys
Pro Gly 1595	Ser Val Gln Pro Leu 1600	Ser Ser Gln Thr Leu 1605	Arg Ala Ser
Ser Ser 1610	Ala Gly Thr Asp Pro 1615	Gln Leu Leu Leu Tyr 1620	Arg Val Val
Arg Gly 1625	Pro Gln Leu Gly Arg 1630	Leu Phe His Ala Gln 1635	Gln Asp Ser
Thr Gly 1640	Glu Ala Leu Val Asn 1645	Phe Thr Gln Ala Glu 1650	Val Tyr Ala
Gly Asn 1655	Ile Leu Tyr Glu His 1660	Glu Met Pro Pro Glu 1665	Pro Phe Trp
Glu Ala 1670	His Asp Thr Leu Glu 1675	Leu Gln Leu Ser Ser 1680	Pro Pro Ala
Arg Asp 1685	Val Ala Ala Thr Leu 1690	Ala Val Ala Val Ser 1695	Phe Glu Ala
Ala Cys 1700	Pro Gln Arg Pro Ser 1705	His Leu Trp Lys Asn 1710	Lys Gly Leu
Trp Val 1715	Pro Glu Gly Gln Arg 1720	Ala Arg Ile Thr Val 1725	Ala Ala Leu
Asp Ala 1730	Ser Asn Leu Leu Ala 1735	Ser Val Pro Ser Pro 1740	Gln Arg Ser
Glu His 1745	Asp Val Leu Phe Gln 1750	Val Thr Gln Phe Pro 1755	Ser Arg Gly
Gln Leu 1760	Leu Val Ser Glu Glu 1765	Pro Leu His Ala Gly 1770	Gln Pro His
Phe Leu 1775	Gln Ser Gln Leu Ala 1780	Ala Gly Gln Leu Val 1785	Tyr Ala His
Gly Gly 1790	Gly Gly Thr Gln Gln 1795	Asp Gly Phe His Phe 1800	Arg Ala His
Leu Gln 1805	Gly Pro Ala Gly Ala 1810	Ser Val Ala Gly Pro 1815	Gln Thr Ser
Glu Ala 1820	Phe Ala Ile Thr Val 1825	Arg Asp Val Asn Glu 1830	Arg Pro Pro
Gln Pro 1835	Gln Ala Ser Val Pro 1840	Leu Arg Leu Thr Arg 1845	Gly Ser Arg
Ala Pro 1850	Ile Ser Arg Ala Gln 1855	Leu Ser Val Val Asp 1860	Pro Asp Ser
Ala Pro 1865	Gly Glu Ile Glu Tyr 1870	Glu Val Gln Arg Ala 1875	Pro His Asn
Gly Phe 1880	Leu Ser Leu Val Gly 1885	Gly Gly Leu Gly Pro 1890	Val Thr Arg

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Phe Thr 1895	Gln Ala Asp Val Asp 1900	Ser Gly Arg Leu Ala 1905	Phe Val Ala
Asn Gly 1910	Ser Ser Val Ala Gly 1915	Ile Phe Gln Leu Ser 1920	Met Ser Asp
Gly Ala 1925	Ser Pro Pro Leu Pro 1930	Met Ser Leu Ala Val 1935	Asp Ile Leu
Pro Ser 1940	Ala Ile Glu Val Gln 1945	Leu Arg Ala Pro Leu 1950	Glu Val Pro
Gln Ala 1955	Leu Gly Arg Ser Ser 1960	Leu Ser Gln Gln Gln 1965	Leu Arg Val
Val Ser 1970	Asp Arg Glu Glu Pro 1975	Glu Ala Ala Tyr Arg 1980	Leu Ile Gln
Gly Pro 1985	Gln Tyr Gly His Leu 1990	Leu Val Gly Gly Arg 1995	Pro Thr Ser
Ala Phe 2000	Ser Gln Phe Gln Ile 2005	Asp Gln Gly Glu Val 2010	Val Phe Ala
Phe Thr 2015	Asn Phe Ser Ser Ser 2020	His Asp His Phe Arg 2025	Val Leu Ala
Leu Ala 2030	Arg Gly Val Asn Ala 2035	Ser Ala Val Val Asn 2040	Val Thr Val
Arg Ala 2045	Leu Leu His Val Trp 2050	Ala Gly Gly Pro Trp 2055	Pro Gln Gly
Ala Thr 2060	Leu Arg Leu Asp Pro 2065	Thr Val Leu Asp Ala 2070	Gly Glu Leu
Ala Asn 2075	Arg Thr Gly Ser Val 2080	Pro Arg Phe Arg Leu 2085	Leu Glu Gly
Pro Arg 2090	His Gly Arg Val Val 2095	Arg Val Pro Arg Ala 2100	Arg Thr Glu
Pro Gly 2105	Gly Ser Gln Leu Val 2110	Glu Gln Phe Thr Gln 2115	Gln Asp Leu
Glu Asp 2120	Gly Arg Leu Gly Leu 2125	Glu Val Gly Arg Pro 2130	Glu Gly Arg
Ala Pro 2135	Gly Pro Ala Gly Asp 2140	Ser Leu Thr Leu Glu 2145	Leu Trp Ala
Gln Gly 2150	Val Pro Pro Ala Val 2155	Ala Ser Leu Asp Phe 2160	Ala Thr Glu
Pro Tyr 2165	Asn Ala Ala Arg Pro 2170	Tyr Ser Val Ala Leu 2175	Leu Ser Val
Pro Glu 2180	Ala Ala Arg Thr Glu 2185	Ala Gly Lys Pro Glu 2190	Ser Ser Thr
Pro Thr 2195	Gly Glu Pro Gly Pro 2200	Met Ala Ser Ser Pro 2205	Glu Pro Ala
Val Ala 2210	Lys Gly Gly Phe Leu 2215	Ser Phe Leu Glu Ala 2220	Asn Met Phe
Ser Val 2225	Ile Ile Pro Met Cys 2230	Leu Val Leu Leu Leu 2235	Leu Ala Leu
Ile Leu 2240	Pro Leu Leu Phe Tyr 2245	Leu Arg Lys Arg Asn 2250	Lys Thr Gly
Lys His 2255	Asp Val Gln Val Leu 2260	Thr Ala Lys Pro Arg 2265	Asn Gly Leu
Ala Gly 2270	Asp Thr Glu Thr Phe 2275	Arg Lys Val Glu Pro 2280	Gly Gln Ala
Ile Pro	Leu Thr Ala Val Pro	Gly Gln Gly Pro Pro	Pro Gly Gly

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2285	2290	2295
Gln Pro Asp Pro Glu Leu Leu Gln Phe Cys Arg Thr Pro Asn Pro		
2300	2305	2310
Ala Leu Lys Asn Gly Gln Tyr Trp Val		
2315	2320	

<210> SEQ ID NO 29
 <211> LENGTH: 931
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 29

Met Asp Met Phe Pro Leu Thr Trp Val Phe Leu Ala Leu Tyr Phe Ser		
1	5	10 15
Arg His Gln Val Arg Gly Gln Pro Asp Pro Pro Cys Gly Gly Arg Leu		
	20	25 30
Asn Ser Lys Asp Ala Gly Tyr Ile Thr Ser Pro Gly Tyr Pro Gln Asp		
	35	40 45
Tyr Pro Ser His Gln Asn Cys Glu Trp Ile Val Tyr Ala Pro Glu Pro		
	50	55 60
Asn Gln Lys Ile Val Leu Asn Phe Asn Pro His Phe Glu Ile Glu Lys		
	65	70 75 80
His Asp Cys Lys Tyr Asp Phe Ile Glu Ile Arg Asp Gly Asp Ser Glu		
	85	90 95
Ser Ala Asp Leu Leu Gly Lys His Cys Gly Asn Ile Ala Pro Pro Thr		
	100	105 110
Ile Ile Ser Ser Gly Ser Met Leu Tyr Ile Lys Phe Thr Ser Asp Tyr		
	115	120 125
Ala Arg Gln Gly Ala Gly Phe Ser Leu Arg Tyr Glu Ile Phe Lys Thr		
	130	135 140
Gly Ser Glu Asp Cys Ser Lys Asn Phe Thr Ser Pro Asn Gly Thr Ile		
	145	150 155 160
Glu Ser Pro Gly Phe Pro Glu Lys Tyr Pro His Asn Leu Asp Cys Thr		
	165	170 175
Phe Thr Ile Leu Ala Lys Pro Lys Met Glu Ile Ile Leu Gln Phe Leu		
	180	185 190
Ile Phe Asp Leu Glu His Asp Pro Leu Gln Val Gly Glu Gly Asp Cys		
	195	200 205
Lys Tyr Asp Trp Leu Asp Ile Trp Asp Gly Ile Pro His Val Gly Pro		
	210	215 220
Leu Ile Gly Lys Tyr Cys Gly Thr Lys Thr Pro Ser Glu Leu Arg Ser		
	225	230 235 240
Ser Thr Gly Ile Leu Ser Leu Thr Phe His Thr Asp Met Ala Val Ala		
	245	250 255
Lys Asp Gly Phe Ser Ala Arg Tyr Tyr Leu Val His Gln Glu Pro Leu		
	260	265 270
Glu Asn Phe Gln Cys Asn Val Pro Leu Gly Met Glu Ser Gly Arg Ile		
	275	280 285
Ala Asn Glu Gln Ile Ser Ala Ser Ser Thr Tyr Ser Asp Gly Arg Trp		
	290	295 300
Thr Pro Gln Gln Ser Arg Leu His Gly Asp Asp Asn Gly Trp Thr Pro		
	305	310 315 320
Asn Leu Asp Ser Asn Lys Glu Tyr Leu Gln Val Asp Leu Arg Phe Leu		
	325	330 335

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Thr	Met	Leu	Thr	Ala	Ile	Ala	Thr	Gln	Gly	Ala	Ile	Ser	Arg	Glu	Thr
			340					345					350		
Gln	Asn	Gly	Tyr	Tyr	Val	Lys	Ser	Tyr	Lys	Leu	Glu	Val	Ser	Thr	Asn
		355					360					365			
Gly	Glu	Asp	Trp	Met	Val	Tyr	Arg	His	Gly	Lys	Asn	His	Lys	Val	Phe
	370					375					380				
Gln	Ala	Asn	Asn	Asp	Ala	Thr	Glu	Val	Val	Leu	Asn	Lys	Leu	His	Ala
	385				390					395					400
Pro	Leu	Leu	Thr	Arg	Phe	Val	Arg	Ile	Arg	Pro	Gln	Thr	Trp	His	Ser
			405						410					415	
Gly	Ile	Ala	Leu	Arg	Leu	Glu	Leu	Phe	Gly	Cys	Arg	Val	Thr	Asp	Ala
			420					425					430		
Pro	Cys	Ser	Asn	Met	Leu	Gly	Met	Leu	Ser	Gly	Leu	Ile	Ala	Asp	Ser
		435					440					445			
Gln	Ile	Ser	Ala	Ser	Ser	Thr	Gln	Glu	Tyr	Leu	Trp	Ser	Pro	Ser	Ala
	450					455					460				
Ala	Arg	Leu	Val	Ser	Ser	Arg	Ser	Gly	Trp	Phe	Pro	Arg	Ile	Pro	Gln
	465				470					475					480
Ala	Gln	Pro	Gly	Glu	Glu	Trp	Leu	Gln	Val	Asp	Leu	Gly	Thr	Pro	Lys
			485					490						495	
Thr	Val	Lys	Gly	Val	Ile	Ile	Gln	Gly	Ala	Arg	Gly	Gly	Asp	Ser	Ile
			500					505					510		
Thr	Ala	Val	Glu	Ala	Arg	Ala	Phe	Val	Arg	Lys	Phe	Lys	Val	Ser	Tyr
		515					520					525			
Ser	Leu	Asn	Gly	Lys	Asp	Trp	Glu	Tyr	Ile	Gln	Asp	Pro	Arg	Thr	Gln
	530					535					540				
Gln	Pro	Lys	Leu	Phe	Glu	Gly	Asn	Met	His	Tyr	Asp	Thr	Pro	Asp	Ile
	545				550					555					560
Arg	Arg	Phe	Asp	Pro	Ile	Pro	Ala	Gln	Tyr	Val	Arg	Val	Tyr	Pro	Glu
			565					570						575	
Arg	Trp	Ser	Pro	Ala	Gly	Ile	Gly	Met	Arg	Leu	Glu	Val	Leu	Gly	Cys
			580					585					590		
Asp	Trp	Thr	Asp	Ser	Lys	Pro	Thr	Val	Glu	Thr	Leu	Gly	Pro	Thr	Val
		595					600					605			
Lys	Ser	Glu	Glu	Thr	Thr	Thr	Pro	Tyr	Pro	Thr	Glu	Glu	Glu	Ala	Thr
	610					615					620				
Glu	Cys	Gly	Glu	Asn	Cys	Ser	Phe	Glu	Asp	Asp	Lys	Asp	Leu	Gln	Leu
	625				630					635					640
Pro	Ser	Gly	Phe	Asn	Cys	Asn	Phe	Asp	Phe	Leu	Glu	Glu	Pro	Cys	Gly
			645					650						655	
Trp	Met	Tyr	Asp	His	Ala	Lys	Trp	Leu	Arg	Thr	Thr	Trp	Ala	Ser	Ser
			660					665					670		
Ser	Ser	Pro	Asn	Asp	Arg	Thr	Phe	Pro	Asp	Asp	Arg	Asn	Phe	Leu	Arg
		675					680					685			
Leu	Gln	Ser	Asp	Ser	Gln	Arg	Glu	Gly	Gln	Tyr	Ala	Arg	Leu	Ile	Ser
	690					695					700				
Pro	Pro	Val	His	Leu	Pro	Arg	Ser	Pro	Val	Cys	Met	Glu	Phe	Gln	Tyr
	705				710					715					720
Gln	Ala	Thr	Gly	Gly	Arg	Gly	Val	Ala	Leu	Gln	Val	Val	Arg	Glu	Ala
			725					730					735		
Ser	Gln	Glu	Ser	Lys	Leu	Leu	Trp	Val	Ile	Arg	Glu	Asp	Gln	Gly	Gly
		740						745				750			
Glu	Trp	Lys	His	Gly	Arg	Ile	Ile	Leu	Pro	Ser	Tyr	Asp	Met	Glu	Tyr

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755	760	765
Gln Ile Val Phe Glu Gly	Val Ile Gly Lys Gly	Arg Ser Gly Glu Ile
770	775	780
Ala Ile Asp Asp Ile Arg	Ile Ser Thr Asp Val	Pro Leu Glu Asn Cys
785	790	795 800
Met Glu Pro Ile Ser Ala	Phe Ala Gly Glu Asn	Phe Lys Val Asp Ile
	805	810 815
Pro Glu Ile His Glu Arg	Glu Gly Tyr Glu Asp	Glu Ile Asp Asp Glu
	820 825	830
Tyr Glu Val Asp Trp Ser	Asn Ser Ser Ser Ala	Thr Ser Gly Ser Gly
	835 840	845
Ala Pro Ser Thr Asp Lys	Glu Lys Ser Trp Leu	Tyr Thr Leu Asp Pro
	850 855	860
Ile Leu Ile Thr Ile Ile	Ala Met Ser Ser Leu	Gly Val Leu Leu Gly
865	870 875	880
Ala Thr Cys Ala Gly Leu	Leu Leu Tyr Cys Thr	Cys Ser Tyr Ser Gly
	885 890	895
Leu Ser Ser Arg Ser Cys	Thr Thr Leu Glu Asn	Tyr Asn Phe Glu Leu
	900 905	910
Tyr Asp Gly Leu Lys His	Lys Val Lys Met Asn	His Gln Lys Cys Cys
	915 920	925
Ser Glu Ala		
930		

<210> SEQ ID NO 30

<211> LENGTH: 750

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 30

Met Trp Asn Leu Leu His	Glu Thr Asp Ser Ala	Val Ala Thr Ala Arg
1	5 10	15
Arg Pro Arg Trp Leu Cys	Ala Gly Ala Leu Val	Leu Ala Gly Gly Phe
	20 25	30
Phe Leu Leu Gly Phe Leu	Phe Gly Trp Phe Ile	Lys Ser Ser Asn Glu
	35 40	45
Ala Thr Asn Ile Thr Pro	Lys His Asn Met Lys	Ala Phe Leu Asp Glu
	50 55	60
Leu Lys Ala Glu Asn Ile	Lys Lys Phe Leu Tyr	Asn Phe Thr Gln Ile
65	70 75	80
Pro His Leu Ala Gly Thr	Glu Gln Asn Phe Gln	Leu Ala Lys Gln Ile
	85 90	95
Gln Ser Gln Trp Lys Glu	Phe Gly Leu Asp Ser	Val Glu Leu Ala His
	100 105	110
Tyr Asp Val Leu Leu Ser	Tyr Pro Asn Lys Thr	His Pro Asn Tyr Ile
	115 120	125
Ser Ile Ile Asn Glu Asp	Gly Asn Glu Ile Phe	Asn Thr Ser Leu Phe
	130 135	140
Glu Pro Pro Pro Pro Gly	Tyr Glu Asn Val Ser	Asp Ile Val Pro Pro
145	150 155	160
Phe Ser Ala Phe Ser Pro	Gln Gly Met Pro Glu	Gly Asp Leu Val Tyr
	165 170	175
Val Asn Tyr Ala Arg Thr	Glu Asp Phe Phe Lys	Leu Glu Arg Asp Met
	180 185	190

Lys	Ile	Asn	Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val
		195					200					205			
Phe	Arg	Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly
		210				215					220				
Val	Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys
225					230					235					240
Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg	Gly
				245					250					255	
Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro	Gly	Tyr
			260					265					270		
Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	Ala	Val	Gly
			275				280					285			
Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	Asp	Ala	Gln	Lys
		290				295					300				
Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	Asp	Ser	Ser	Trp	Arg
305					310					315					320
Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	Pro	Gly	Phe	Thr	Gly	Asn
				325					330					335	
Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	Ile	His	Ser	Thr	Asn	Glu	Val
			340					345					350		
Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro
			355				360					365			
Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly
		370				375					380				
Gly	Ile	Asp	Pro	Gln	Ser	Gly	Ala	Ala	Val	Val	His	Glu	Ile	Val	Arg
385					390					395					400
Ser	Phe	Gly	Thr	Leu	Lys	Lys	Glu	Gly	Trp	Arg	Pro	Arg	Arg	Thr	Ile
				405					410					415	
Leu	Phe	Ala	Ser	Trp	Asp	Ala	Glu	Glu	Phe	Gly	Leu	Leu	Gly	Ser	Thr
			420					425					430		
Glu	Trp	Ala	Glu	Glu	Asn	Ser	Arg	Leu	Leu	Gln	Glu	Arg	Gly	Val	Ala
				435			440					445			
Tyr	Ile	Asn	Ala	Asp	Ser	Ser	Ile	Glu	Gly	Asn	Tyr	Thr	Leu	Arg	Val
		450				455					460				
Asp	Cys	Thr	Pro	Leu	Met	Tyr	Ser	Leu	Val	His	Asn	Leu	Thr	Lys	Glu
465					470					475					480
Leu	Lys	Ser	Pro	Asp	Glu	Gly	Phe	Glu	Gly	Lys	Ser	Leu	Tyr	Glu	Ser
				485					490					495	
Trp	Thr	Lys	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ser	Gly	Met	Pro	Arg	Ile
			500					505					510		
Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe	Gln	Arg	Leu
		515					520					525			
Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn	Trp	Glu	Thr	Asn
		530				535						540			
Lys	Phe	Ser	Gly	Tyr	Pro	Leu	Tyr								

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610	615	620
Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr		
625	630	635 640
Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser		
	645	650 655
Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu		
	660	665 670
Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg		
	675	680 685
His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser		
	690	695 700
Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp		
	705	710 715 720
Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala		
	725	730 735
Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala		
	740	745 750

<210> SEQ ID NO 31
 <211> LENGTH: 1338
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 31

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser		
1	5	10 15
Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro		
	20	25 30
Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr		
	35	40 45
Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro		
	50	55 60
Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala		
	65	70 75 80
Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr		
	85	90 95
Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val		
	100	105 110
Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile		
	115	120 125
Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu		
	130	135 140
Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val		
	145	150 155 160
Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr		
	165	170 175
Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe		
	180	185 190
Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu		
	195	200 205
Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg		
	210	215 220
Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val		
	225	230 235 240

Lys	Leu	Leu	Arg	Gly	His	Thr	Leu	Val	Leu	Asn	Cys	Thr	Ala	Thr	Thr	
				245					250					255		
Pro	Leu	Asn	Thr	Arg	Val	Gln	Met	Thr	Trp	Ser	Tyr	Pro	Asp	Glu	Lys	
				260					265					270		
Asn	Lys	Arg	Ala	Ser	Val	Arg	Arg	Arg	Ile	Asp	Gln	Ser	Asn	Ser	His	
				275					280					285		
Ala	Asn	Ile	Phe	Tyr	Ser	Val	Leu	Thr	Ile	Asp	Lys	Met	Gln	Asn	Lys	
				290					295					300		
Asp	Lys	Gly	Leu	Tyr	Thr	Cys	Arg	Val	Arg	Ser	Gly	Pro	Ser	Phe	Lys	
				305					310					315		
Ser	Val	Asn	Thr	Ser	Val	His	Ile	Tyr	Asp	Lys	Ala	Phe	Ile	Thr	Val	
				325					330					335		
Lys	His	Arg	Lys	Gln	Gln	Val	Leu	Glu	Thr	Val	Ala	Gly	Lys	Arg	Ser	
				340					345					350		
Tyr	Arg	Leu	Ser	Met	Lys	Val	Lys	Ala	Phe	Pro	Ser	Pro	Glu	Val	Val	
				355					360					365		
Trp	Leu	Lys	Asp	Gly	Leu	Pro	Ala	Thr	Glu	Lys	Ser	Ala	Arg	Tyr	Leu	
				370					375					380		
Thr	Arg	Gly	Tyr	Ser	Leu	Ile	Ile	Lys	Asp	Val	Thr	Glu	Glu	Asp	Ala	
				385					390					395		
Gly	Asn	Tyr	Thr	Ile	Leu	Leu	Ser	Ile	Lys	Gln	Ser	Asn	Val	Phe	Lys	
				405					410					415		
Asn	Leu	Thr	Ala	Thr	Leu	Ile	Val	Asn	Val	Lys	Pro	Gln	Ile	Tyr	Glu	
				420					425					430		
Lys	Ala	Val	Ser	Ser	Phe	Pro	Asp	Pro	Ala	Leu	Tyr	Pro	Leu	Gly	Ser	
				435					440					445		
Arg	Gln	Ile	Leu	Thr	Cys	Thr	Ala	Tyr	Gly	Ile	Pro	Gln	Pro	Thr	Ile	
				450					455					460		
Lys	Trp	Phe	Trp	His	Pro	Cys	Asn	His	Asn	His	Ser	Glu	Ala	Arg	Cys	
				465					470					475		
Asp	Phe	Cys	Ser	Asn	Asn	Glu	Glu	Ser	Phe	Ile	Leu	Asp	Ala	Asp	Ser	
				485					490					495		
Asn	Met	Gly	Asn	Arg	Ile	Glu	Ser	Ile	Thr	Gln	Arg	Met	Ala	Ile	Ile	
				500					505					510		
Glu	Gly	Lys	Asn	Lys	Met	Ala	Ser	Thr	Leu	Val	Val	Ala	Asp	Ser	Arg	
				515					520					525		
Ile	Ser	Gly	Ile	Tyr	Ile	Cys	Ile	Ala	Ser	Asn	Lys	Val	Gly	Thr	Val	
				530					535					540		
Gly	Arg	Asn	Ile	Ser	Phe	Tyr	Ile	Thr	Asp	Val	Pro	Asn	Gly	Phe	His	
				545					550					555		
Val	Asn	Leu	Glu	Lys	Met	Pro	Thr	Glu	Gly	Glu	Asp	Leu	Lys	Leu	Ser	
				565					570					575		
Cys	Thr	Val	Asn	Lys	Phe	Leu	Tyr	Arg	Asp	Val	Thr	Trp	Ile	Leu	Leu	
				580					585					590		
Arg	Thr	Val	Asn	Asn	Arg	Thr	Met	His	Tyr	Ser	Ile	Ser	Lys	Gln	Lys	
				595					600					605		
Met	Ala	Ile	Thr	Lys	Glu	His	Ser	Ile	Thr	Leu	Asn	Leu	Thr	Ile	Met	
				610					615					620		
Asn	Val	Ser	Leu	Gln	Asp	Ser	Gly	Thr	Tyr	Ala	Cys	Arg	Ala	Arg	Asn	
				625					630					635		
Val	Tyr	Thr	Gly	Glu	Glu	Ile	Leu	Gln	Lys	Lys	Glu	Ile	Thr	Ile</		

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660	665	670
Ala Ile Ser Ser Ser Thr Thr	Leu Asp Cys His Ala Asn Gly Val Pro	
675	680	685
Glu Pro Gln Ile Thr Trp Phe	Lys Asn Asn His Lys Ile Gln Gln Glu	
690	695	700
Pro Gly Ile Ile Leu Gly Pro	Gly Ser Ser Thr Leu Phe Ile Glu Arg	
705	710	715
Val Thr Glu Glu Asp Glu Gly	Val Tyr His Cys Lys Ala Thr Asn Gln	
725	730	735
Lys Gly Ser Val Glu Ser Ser	Ala Tyr Leu Thr Val Gln Gly Thr Ser	
740	745	750
Asp Lys Ser Asn Leu Glu Leu	Ile Thr Leu Thr Cys Thr Cys Val Ala	
755	760	765
Ala Thr Leu Phe Trp Leu Leu	Leu Thr Leu Phe Ile Arg Lys Met Lys	
770	775	780
Arg Ser Ser Ser Glu Ile Lys	Thr Asp Tyr Leu Ser Ile Ile Met Asp	
785	790	795
Pro Asp Glu Val Pro Leu Asp	Glu Gln Cys Glu Arg Leu Pro Tyr Asp	
805	810	815
Ala Ser Lys Trp Glu Phe Ala	Arg Glu Arg Leu Lys Leu Gly Lys Ser	
820	825	830
Leu Gly Arg Gly Ala Phe Gly	Lys Val Val Gln Ala Ser Ala Phe Gly	
835	840	845
Ile Lys Lys Ser Pro Thr Cys	Arg Thr Val Ala Val Lys Met Leu Lys	
850	855	860
Glu Gly Ala Thr Ala Ser Glu	Tyr Lys Ala Leu Met Thr Glu Leu Lys	
865	870	875
Ile Leu Thr His Ile Gly His	His Leu Asn Val Val Asn Leu Leu Gly	
885	890	895
Ala Cys Thr Lys Gln Gly Gly	Pro Leu Met Val Ile Val Glu Tyr Cys	
900	905	910
Lys Tyr Gly Asn Leu Ser Asn	Tyr Leu Lys Ser Lys Arg Asp Leu Phe	
915	920	925
Phe Leu Asn Lys Asp Ala Ala	Leu His Met Glu Pro Lys Lys Glu Lys	
930	935	940
Met Glu Pro Gly Leu Glu Gln	Gly Lys Lys Pro Arg Leu Asp Ser Val	
945	950	955
Thr Ser Ser Glu Ser Phe Ala	Ser Ser Gly Phe Gln Glu Asp Lys Ser	
965	970	975
Leu Ser Asp Val Glu Glu Glu	Glu Asp Ser Asp Gly Phe Tyr Lys Glu	
980	985	990
Pro Ile Thr Met Glu Asp Leu	Ile Ser Tyr Ser Phe Gln Val Ala Arg	
995	1000	1005
Gly Met Glu Phe Leu Ser Ser	Arg Lys Cys Ile His Arg Asp Leu	
1010	1015	1020
Ala Ala Arg Asn Ile Leu Leu	Ser Glu Asn Asn Val Val Lys Ile	
1025	1030	1035
Cys Asp Phe Gly Leu Ala Arg	Asp Ile Tyr Lys Asn Pro Asp Tyr	
1040	1045	1050
Val Arg Lys Gly Asp Thr Arg	Leu Pro Leu Lys Trp Met Ala Pro	
1055	1060	1065
Glu Ser Ile Phe Asp Lys Ile	Tyr Ser Thr Lys Ser Asp Val Trp	
1070	1075	1080

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Ser	Tyr	Gly	Val	Leu	Leu	Trp	Glu	Ile	Phe	Ser	Leu	Gly	Gly	Ser
1085						1090						1095		
Pro	Tyr	Pro	Gly	Val	Gln	Met	Asp	Glu	Asp	Phe	Cys	Ser	Arg	Leu
1100						1105						1110		
Arg	Glu	Gly	Met	Arg	Met	Arg	Ala	Pro	Glu	Tyr	Ser	Thr	Pro	Glu
1115						1120						1125		
Ile	Tyr	Gln	Ile	Met	Leu	Asp	Cys	Trp	His	Arg	Asp	Pro	Lys	Glu
1130						1135						1140		
Arg	Pro	Arg	Phe	Ala	Glu	Leu	Val	Glu	Lys	Leu	Gly	Asp	Leu	Leu
1145						1150						1155		
Gln	Ala	Asn	Val	Gln	Gln	Asp	Gly	Lys	Asp	Tyr	Ile	Pro	Ile	Asn
1160						1165						1170		
Ala	Ile	Leu	Thr	Gly	Asn	Ser	Gly	Phe	Thr	Tyr	Ser	Thr	Pro	Ala
1175						1180						1185		
Phe	Ser	Glu	Asp	Phe	Phe	Lys	Glu	Ser	Ile	Ser	Ala	Pro	Lys	Phe
1190						1195						1200		
Asn	Ser	Gly	Ser	Ser	Asp	Asp	Val	Arg	Tyr	Val	Asn	Ala	Phe	Lys
1205						1210						1215		
Phe	Met	Ser	Leu	Glu	Arg	Ile	Lys	Thr	Phe	Glu	Glu	Leu	Leu	Pro
1220						1225						1230		
Asn	Ala	Thr	Ser	Met	Phe	Asp	Asp	Tyr	Gln	Gly	Asp	Ser	Ser	Thr
1235						1240						1245		
Leu	Leu	Ala	Ser	Pro	Met	Leu	Lys	Arg	Phe	Thr	Trp	Thr	Asp	Ser
1250						1255						1260		
Lys	Pro	Lys	Ala	Ser	Leu	Lys	Ile	Asp	Leu	Arg	Val	Thr	Ser	Lys
1265						1270						1275		
Ser	Lys	Glu	Ser	Gly	Leu	Ser	Asp	Val	Ser	Arg	Pro	Ser	Phe	Cys
1280						1285						1290		
His	Ser	Ser	Cys	Gly	His	Val	Ser	Glu	Gly	Lys	Arg	Arg	Phe	Thr
1295						1300						1305		
Tyr	Asp	His	Ala	Glu	Leu	Glu	Arg	Lys	Ile	Ala	Cys	Cys	Ser	Pro
1310						1315						1320		
Pro	Pro	Asp	Tyr	Asn	Ser	Val	Val	Leu	Tyr	Ser	Thr	Pro	Pro	Ile
1325						1330						1335		

<210> SEQ ID NO 32

<211> LENGTH: 1356

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 32

Met	Gln	Ser	Lys	Val	Leu	Leu	Ala	Val	Ala	Leu	Trp	Leu	Cys	Val	Glu
1			5						10				15		
Thr	Arg	Ala	Ala	Ser	Val	Gly	Leu	Pro	Ser	Val	Ser	Leu	Asp	Leu	Pro
		20						25					30		
Arg	Leu	Ser	Ile	Gln	Lys	Asp	Ile	Leu	Thr	Ile	Lys	Ala	Asn	Thr	Thr
		35					40					45			
Leu	Gln	Ile	Thr	Cys	Arg	Gly	Gln	Arg	Asp	Leu	Asp	Trp	Leu	Trp	Pro
		50				55					60				
Asn	Asn	Gln	Ser	Gly	Ser	Glu	Gln	Arg	Val	Glu	Val	Thr	Glu	Cys	Ser
65					70					75				80	
Asp	Gly	Leu	Phe	Cys	Lys	Thr	Leu	Thr	Ile	Pro	Lys	Val	Ile	Gly	Asn
			85					90						95	
Asp	Thr	Gly	Ala	Tyr	Lys	Cys	Phe	Tyr	Arg	Glu	Thr	Asp	Leu	Ala	Ser

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100						105						110					
Val	Ile	Tyr	Val	Tyr	Val	Gln	Asp	Tyr	Arg	Ser	Pro	Phe	Ile	Ala	Ser		
115						120						125					
Val	Ser	Asp	Gln	His	Gly	Val	Val	Tyr	Ile	Thr	Glu	Asn	Lys	Asn	Lys		
130						135						140					
Thr	Val	Val	Ile	Pro	Cys	Leu	Gly	Ser	Ile	Ser	Asn	Leu	Asn	Val	Ser		
145			150						155			160					
Leu	Cys	Ala	Arg	Tyr	Pro	Glu	Lys	Arg	Phe	Val	Pro	Asp	Gly	Asn	Arg		
			165						170			175					
Ile	Ser	Trp	Asp	Ser	Lys	Lys	Gly	Phe	Thr	Ile	Pro	Ser	Tyr	Met	Ile		
			180						185			190					
Ser	Tyr	Ala	Gly	Met	Val	Phe	Cys	Glu	Ala	Lys	Ile	Asn	Asp	Glu	Ser		
			195			200						205					
Tyr	Gln	Ser	Ile	Met	Tyr	Ile	Val	Val	Val	Val	Gly	Tyr	Arg	Ile	Tyr		
210						215						220					
Asp	Val	Val	Leu	Ser	Pro	Ser	His	Gly	Ile	Glu	Leu	Ser	Val	Gly	Glu		
225						230			235			240					
Lys	Leu	Val	Leu	Asn	Cys	Thr	Ala	Arg	Thr	Glu	Leu	Asn	Val	Gly	Ile		
			245						250			255					
Asp	Phe	Asn	Trp	Glu	Tyr	Pro	Ser	Ser	Lys	His	Gln	His	Lys	Lys	Leu		
			260						265			270					
Val	Asn	Arg	Asp	Leu	Lys	Thr	Gln	Ser	Gly	Ser	Glu	Met	Lys	Lys	Phe		
			275			280						285					
Leu	Ser	Thr	Leu	Thr	Ile	Asp	Gly	Val	Thr	Arg	Ser	Asp	Gln	Gly	Leu		
290						295						300					
Tyr	Thr	Cys	Ala	Ala	Ser	Ser	Gly	Leu	Met	Thr	Lys	Lys	Asn	Ser	Thr		
305						310			315			320					
Phe	Val	Arg	Val	His	Glu	Lys	Pro	Phe	Val	Ala	Phe	Gly	Ser	Gly	Met		
			325						330			335					
Glu	Ser	Leu	Val	Glu	Ala	Thr	Val	Gly	Glu	Arg	Val	Arg	Ile	Pro	Ala		
			340						345			350					
Lys	Tyr	Leu	Gly	Tyr	Pro	Pro	Pro	Glu	Ile	Lys	Trp	Tyr	Lys	Asn	Gly		
			355						360			365					
Ile	Pro	Leu	Glu	Ser	Asn	His	Thr	Ile	Lys	Ala	Gly	His	Val	Leu	Thr		
			370			375						380					
Ile	Met	Glu	Val	Ser	Glu	Arg	Asp	Thr	Gly	Asn	Tyr	Thr	Val	Ile	Leu		
385						390			395			400					
Thr	Asn	Pro	Ile	Ser	Lys	Glu	Lys	Gln	Ser	His	Val	Val	Ser	Leu	Val		
			405						410			415					
Val	Tyr	Val	Pro	Pro	Gln	Ile	Gly	Glu	Lys	Ser	Leu	Ile	Ser	Pro	Val		
			420						425			430					
Asp	Ser	Tyr	Gln	Tyr	Gly	Thr	Thr	Gln	Thr	Leu	Thr	Cys	Thr	Val	Tyr		
			435						440			445					
Ala	Ile	Pro	Pro	Pro	His	His	Ile	His	Trp	Tyr	Trp	Gln	Leu	Glu	Glu		
			450			455						460					
Glu	Cys	Ala	Asn	Glu	Pro	Ser	Gln	Ala	Val	Ser	Val	Thr	Asn	Pro	Tyr		
465						470			475			480					
Pro	Cys	Glu	Glu	Trp	Arg	Ser	Val	Glu	Asp	Phe	Gln	Gly	Gly	Asn	Lys		
			485						490			495					
Ile	Glu	Val	Asn	Lys	Asn	Gln	Phe	Ala	Leu	Ile	Glu	Gly	Lys	Asn	Lys		
			500						505			510					
Thr	Val	Ser	Thr	Leu	Val	Ile	Gln	Ala	Ala	Asn	Val	Ser	Ala	Leu	Tyr		
			515			520						525					

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Lys	Cys	Glu	Ala	Val	Asn	Lys	Val	Gly	Arg	Gly	Glu	Arg	Val	Ile	Ser
530						535					540				
Phe	His	Val	Thr	Arg	Gly	Pro	Glu	Ile	Thr	Leu	Gln	Pro	Asp	Met	Gln
545					550					555					560
Pro	Thr	Glu	Gln	Glu	Ser	Val	Ser	Leu	Trp	Cys	Thr	Ala	Asp	Arg	Ser
					565				570					575	
Thr	Phe	Glu	Asn	Leu	Thr	Trp	Tyr	Lys	Leu	Gly	Pro	Gln	Pro	Leu	Pro
			580					585					590		
Ile	His	Val	Gly	Glu	Leu	Pro	Thr	Pro	Val	Cys	Lys	Asn	Leu	Asp	Thr
			595				600					605			
Leu	Trp	Lys	Leu	Asn	Ala	Thr	Met	Phe	Ser	Asn	Ser	Thr	Asn	Asp	Ile
610						615					620				
Leu	Ile	Met	Glu	Leu	Lys	Asn	Ala	Ser	Leu	Gln	Asp	Gln	Gly	Asp	Tyr
625					630					635					640
Val	Cys	Leu	Ala	Gln	Asp	Arg	Lys	Thr	Lys	Lys	Arg	His	Cys	Val	Val
				645					650					655	
Arg	Gln	Leu	Thr	Val	Leu	Glu	Arg	Val	Ala	Pro	Thr	Ile	Thr	Gly	Asn
				660				665					670		
Leu	Glu	Asn	Gln	Thr	Thr	Ser	Ile	Gly	Glu	Ser	Ile	Glu	Val	Ser	Cys
		675				680					685				
Thr	Ala	Ser	Gly	Asn	Pro	Pro	Pro	Gln	Ile	Met	Trp	Phe	Lys	Asp	Asn
690					695						700				
Glu	Thr	Leu	Val	Glu	Asp	Ser	Gly	Ile	Val	Leu	Lys	Asp	Gly	Asn	Arg
705					710					715					720
Asn	Leu	Thr	Ile	Arg	Arg	Val	Arg	Lys	Glu	Asp	Glu	Gly	Leu	Tyr	Thr
				725				730					735		
Cys	Gln	Ala	Cys	Ser	Val	Leu	Gly	Cys	Ala	Lys	Val	Glu	Ala	Phe	Phe
			740					745					750		
Ile	Ile	Glu	Gly	Ala	Gln	Glu	Lys	Thr	Asn	Leu	Glu	Ile	Ile	Ile	Leu
		755					760					765			
Val	Gly	Thr	Ala	Val	Ile	Ala	Met	Phe	Phe	Trp	Leu	Leu	Leu	Val	Ile
	770					775					780				
Ile	Leu	Arg	Thr	Val	Lys	Arg	Ala	Asn	Gly	Gly	Glu	Leu	Lys	Thr	Gly
785					790					795					800
Tyr	Leu	Ser	Ile	Val	Met	Asp	Pro	Asp	Glu	Leu	Pro	Leu	Asp	Glu	His
				805				810						815	
Cys	Glu	Arg	Leu	Pro	Tyr	Asp	Ala	Ser	Lys	Trp	Glu	Phe	Pro	Arg	Asp
			820					825					830		
Arg	Leu	Lys	Leu	Gly	Lys	Pro	Leu	Gly	Arg	Gly	Ala	Phe	Gly	Gln	Val
		835					840					845			
Ile	Glu	Ala	Asp	Ala	Phe	Gly	Ile	Asp	Lys	Thr	Ala	Thr	Cys	Arg	Thr
	850					855					860				
Val	Ala	Val	Lys	Met	Leu	Lys	Glu	Gly	Ala	Thr	His	Ser	Glu	His	Arg
865					870					875					880
Ala	Leu	Met	Ser	Glu	Leu	Lys	Ile	Leu	Ile	His	Ile	Gly	His	His	Leu
				885				890						895	
Asn	Val	Val	Asn	Leu	Leu	Gly	Ala	Cys	Thr	Lys	Pro	Gly	Gly	Pro	Leu
			900					905					910		
Met	Val	Ile	Val	Glu	Phe	Cys	Lys	Phe	Gly	Asn	Leu	Ser	Thr	Tyr	Leu
		915					920						925		
Arg	Ser	Lys	Arg	Asn	Glu	Phe	Val	Pro	Tyr	Lys	Thr	Lys	Gly	Ala	Arg
	930						935						940		

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Phe	Arg	Gln	Gly	Lys	Asp	Tyr	Val	Gly	Ala	Ile	Pro	Val	Asp	Leu	Lys	945	950	955	960
Arg	Arg	Leu	Asp	Ser	Ile	Thr	Ser	Ser	Gln	Ser	Ser	Ala	Ser	Ser	Gly	965	970	975	
Phe	Val	Glu	Glu	Lys	Ser	Leu	Ser	Asp	Val	Glu	Glu	Glu	Glu	Ala	Pro	980	985	990	
Glu	Asp	Leu	Tyr	Lys	Asp	Phe	Leu	Thr	Leu	Glu	His	Leu	Ile	Cys	Tyr	995	1000	1005	
Ser	Phe	Gln	Val	Ala	Lys	Gly	Met	Glu	Phe	Leu	Ala	Ser	Arg	Lys		1010	1015	1020	
Cys	Ile	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Leu	Ser	Glu		1025	1030	1035	
Lys	Asn	Val	Val	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Asp	Ile		1040	1045	1050	
Tyr	Lys	Asp	Pro	Asp	Tyr	Val	Arg	Lys	Gly	Asp	Ala	Arg	Leu	Pro		1055	1060	1065	
Leu	Lys	Trp	Met	Ala	Pro	Glu	Thr	Ile	Phe	Asp	Arg	Val	Tyr	Thr		1070	1075	1080	
Ile	Gln	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Leu	Leu	Trp	Glu	Ile		1085	1090	1095	
Phe	Ser	Leu	Gly	Ala	Ser	Pro	Tyr	Pro	Gly	Val	Lys	Ile	Asp	Glu		1100	1105	1110	
Glu	Phe	Cys	Arg	Arg	Leu	Lys	Glu	Gly	Thr	Arg	Met	Arg	Ala	Pro		1115	1120	1125	
Asp	Tyr	Thr	Thr	Pro	Glu	Met	Tyr	Gln	Thr	Met	Leu	Asp	Cys	Trp		1130	1135	1140	
His	Gly	Glu	Pro	Ser	Gln	Arg	Pro	Thr	Phe	Ser	Glu	Leu	Val	Glu		1145	1150	1155	
His	Leu	Gly	Asn	Leu	Leu	Gln	Ala	Asn	Ala	Gln	Gln	Asp	Gly	Lys		1160	1165	1170	
Asp	Tyr	Ile	Val	Leu	Pro	Ile	Ser	Glu	Thr	Leu	Ser	Met	Glu	Glu		1175	1180	1185	
Asp	Ser	Gly	Leu	Ser	Leu	Pro	Thr	Ser	Pro	Val	Ser	Cys	Met	Glu		1190	1195	1200	
Glu	Glu	Glu	Val	Cys	Asp	Pro	Lys	Phe	His	Tyr	Asp	Asn	Thr	Ala		1205	1210	1215	
Gly	Ile	Ser	Gln	Tyr	Leu	Gln	Asn	Ser	Lys	Arg	Lys	Ser	Arg	Pro		1220	1225	1230	
Val	Ser	Val	Lys	Thr	Phe	Glu	Asp	Ile	Pro	Leu	Glu	Glu	Pro	Glu		1235	1240	1245	
Val	Lys	Val	Ile	Pro	Asp	Asp	Asn	Gln	Thr	Asp	Ser	Gly	Met	Val		1250	1255	1260	
Leu	Ala	Ser	Glu	Glu	Leu	Lys	Thr	Leu	Glu	Asp	Arg	Thr	Lys	Leu		1265	1270	1275	
Ser	Pro	Ser	Phe	Gly	Gly	Met	Val	Pro	Ser	Lys	Ser	Arg	Glu	Ser		1280	1285	1290	
Val	Ala	Ser	Glu	Gly	Ser	Asn	Gln	Thr	Ser	Gly	Tyr	Gln	Ser	Gly		1295	1300	1305	
Tyr	His	Ser	Asp	Asp	Thr	Asp	Thr	Thr	Val	Tyr	Ser	Ser	Glu	Glu		1310	1315	1320	
Ala	Glu	Leu	Leu	Lys	Leu	Ile	Glu	Ile	Gly	Val	Gln	Thr	Gly	Ser		1325	1330	1335	
Thr	Ala	Gln	Ile	Leu	Gln	Pro	Asp	Ser	Gly	Thr	Thr	Leu	Ser	Ser					

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1340	1345	1350
Pro Pro Val		
1355		
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<211> LENGTH: 20		
<212> TYPE: DNA		
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<400> SEQUENCE: 33		
agcccaccag agacatggaa		20
<210> SEQ ID NO 34		
<211> LENGTH: 20		
<212> TYPE: DNA		
<213> ORGANISM: Homo sapiens		
<400> SEQUENCE: 34		
ctggctctgt tggaggctgt		20
<210> SEQ ID NO 35		
<211> LENGTH: 20		
<212> TYPE: DNA		
<213> ORGANISM: Homo sapiens		
<400> SEQUENCE: 35		
ctgcacacct gggttctctg		20
<210> SEQ ID NO 36		
<211> LENGTH: 20		
<212> TYPE: DNA		
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<400> SEQUENCE: 36		
gcatgggtta ggggtacagc		20
<210> SEQ ID NO 37		
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<212> TYPE: DNA		
<213> ORGANISM: Homo sapiens		
<400> SEQUENCE: 37		
ggggatgcca acagctataa		20
<210> SEQ ID NO 38		
<211> LENGTH: 20		
<212> TYPE: DNA		
<213> ORGANISM: Homo sapiens		
<400> SEQUENCE: 38		
ctcctgccag taccagaagc		20
<210> SEQ ID NO 39		
<211> LENGTH: 20		
<212> TYPE: DNA		
<213> ORGANISM: Homo sapiens		
<400> SEQUENCE: 39		
catcaatggg agccaggtgt		20
<210> SEQ ID NO 40		
<211> LENGTH: 20		
<212> TYPE: DNA		

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 40

tgaaggttga actggcgtga 20

<210> SEQ ID NO 41

<211> LENGTH: 22

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 41

tcagaaacag acatcatggt gc 22

<210> SEQ ID NO 42

<211> LENGTH: 22

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 42

tagacaatag cagaaaaggg gc 22

<210> SEQ ID NO 43

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 43

acagacgcct ttgttctgct 20

<210> SEQ ID NO 44

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 44

tcggaagaaa tgtccaggag 20

<210> SEQ ID NO 45

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 45

tccaagtgga cctgggagat 20

<210> SEQ ID NO 46

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 46

ttcacagccc agtagtcca 20

<210> SEQ ID NO 47

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 47

ccggaagaga cctgtggttg 20

<210> SEQ ID NO 48

<211> LENGTH: 20

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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 48
ccgatacgtcc cttccctatc 20

<210> SEQ ID NO 49
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 49
tgctcctgga gaggcctctg 20

<210> SEQ ID NO 50
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 50
ggaggaagtg ttgacttcat tc 22

<210> SEQ ID NO 51
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 51
cctgcggtga agtcctatcc 20

<210> SEQ ID NO 52
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 52
gtttccagca aagccaggtc 20

<210> SEQ ID NO 53
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 53
aagttgggaa ttctcctcca g 21

<210> SEQ ID NO 54
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 54
ttcctcactg aattcagact tc 22

<210> SEQ ID NO 55
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 55
ttcaccaact gggcccagc 19

<210> SEQ ID NO 56

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<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 56

gttgacacac atctgctggc 20

<210> SEQ ID NO 57
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 57

ccaactacct caagagcaaa c 21

<210> SEQ ID NO 58
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 58

ccaggtcccg atgaatgcac 20

<210> SEQ ID NO 59
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 59

acagacagtg ggatggtcc 19

<210> SEQ ID NO 60
<211> LENGTH: 19
<212> TYPE: DNA
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<400> SEQUENCE: 60

aaacaggagg tgagcgag 19

<210> SEQ ID NO 61
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<400> SEQUENCE: 61

ggcatcgtga tggactccg 19

<210> SEQ ID NO 62
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 62

gctggaaggt ggacagcga 19

<210> SEQ ID NO 63
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 63

tgtgaccccc agtatggatt 20

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<210> SEQ ID NO 64
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 64

ccaggggcag ttacacactt

20

<210> SEQ ID NO 65
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 65

Cys Pro Pro Gly Phe Ser Gly Asn Phe
1 5

<210> SEQ ID NO 66
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 66

Gly Phe Ser Gly Asn Phe Cys Glu Ile
1 5

<210> SEQ ID NO 67
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 67

Thr Ile Leu Gly Val Leu Thr Ser Leu Val Val Leu
1 5 10

<210> SEQ ID NO 68
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 68

Arg Leu Thr Pro Gly Val His Glu Leu
1 5

<210> SEQ ID NO 69
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 69

Arg Leu Thr Pro Gly Val His Glu Val
1 5

<210> SEQ ID NO 70
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 70

Arg Leu Leu Val Val Tyr Pro Trp Thr
1 5

<210> SEQ ID NO 71
<211> LENGTH: 9
<212> TYPE: PRT

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 71

Arg Leu Leu Val Val Tyr Pro Trp Val
1 5

<210> SEQ ID NO 72

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 72

Arg Leu Leu Gly Asn Val Leu Val Cys Val
1 5 10

<210> SEQ ID NO 73

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 73

Arg Leu Leu Gly Asn Val Leu Val Val Val
1 5 10

<210> SEQ ID NO 74

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 74

Gly Leu Leu Gly Met Val Ser Gly Leu
1 5

<210> SEQ ID NO 75

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 75

Gly Met Leu Gly Met Val Ser Gly Leu
1 5

<210> SEQ ID NO 76

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 76

Leu Leu Val Pro Thr Cys Val Phe Leu Val
1 5 10

<210> SEQ ID NO 77

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 77

Leu Leu Val Pro Thr Cys Val Phe Val Val
1 5 10

<210> SEQ ID NO 78

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 78

Leu Leu Ala Leu Pro His Ser Cys Leu
1 5

<210> SEQ ID NO 79

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 79

Leu Ala Ala Leu Pro His Ser Cys Leu
1 5

<210> SEQ ID NO 80

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 80

Ile Leu Leu Trp Glu Ile Phe Thr Val
1 5

<210> SEQ ID NO 81

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 81

Ile Leu Leu Trp Glu Ile Phe Thr Leu
1 5

<210> SEQ ID NO 82

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 82

Ile Leu Ser Asn Leu Ser Phe Pro Val
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<210> SEQ ID NO 83

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 83

Thr Leu Ser Asn Leu Ser Phe Pro Val
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<210> SEQ ID NO 84

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Linker

<400> SEQUENCE: 84

Gly Gly Gly Gly Ser
1 5

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We claim:

1. A method for eliciting an immune response to a tumor in a subject, comprising administering to a subject a therapeutically effective amount of

a composition comprising a plurality of polypeptides, wherein each polypeptide in the plurality is at most twelve amino acids in length, wherein the plurality of polypeptides comprises:

(a) a Protein Delta Homolog 1 (DLK1) polypeptide comprising the amino acid sequence set forth as ILGV-LTSLV (SEQ ID NO: 2);

(b) a Neuropilin 1 (NRP1) polypeptide comprising the amino acid sequence set forth as GX₄LGMVSG (SEQ ID NO: 7), wherein X₄ is a leucine (L) or a methionine (M); and

(c) a Tumor Endothelial Marker 1 (TEM1) polypeptide comprising the amino acid sequence set forth as LLVPTCVFX₅V (SEQ ID NO: 9), wherein X₅ is a leucine (L) or a valine (V),

thereby eliciting the immune response to the tumor in the subject, wherein the tumor expresses DLK1, NRP1 and TEM1.

2. The method of claim 1, further comprising administering to the subject a therapeutically effective amount of dasatinib, bevacizumab, sunitinib, axitinib, an HSP90 inhibitor, or gemcitabine/fludarabine.

3. The method of claim 1, wherein the immune response decreases growth of the tumor in the subject.

4. The method of claim 1, wherein the immune response decreases vascularization of the tumor.

5. The method of claim 1, wherein the tumor is a colorectal cancer.

6. The method of claim 1, wherein the plurality of polypeptides comprises:

(a) a Protein Delta Homolog 1 (DLK1) polypeptide comprising the amino acid sequence set forth as ILGV-LTSLV (SEQ ID NO: 2);

(b) a Neuropilin 1 (NRP1) polypeptide comprising the amino acid sequence set forth as GX₄LGMVSG (SEQ ID NO: 7), wherein X₄ is a methionine (M); and

(c) a Tumor Endothelial Marker 1 (TEM1) polypeptide comprising the amino acid sequence set forth as LLVPTCVFX₅V (SEQ ID NO: 9), wherein X₅ is a leucine (L).

7. The method of claim 1, wherein the cancer is a lung cancer.

8. A method for inhibiting the growth of a cancer, the method comprising

culturing cytotoxic T lymphocytes (CTLs) or CTL precursor cells with a composition and an antigen presenting cell in vitro to produce activated CTLs or CTL matured from the CTL precursors that recognize tumor associated stromal cell antigens, wherein the composition comprises a plurality of polypeptides, wherein each polypeptide in the plurality is at most twelve amino acids in length, wherein the plurality of polypeptides comprises:

(a) a Protein Delta Homolog 1 (DLK1) polypeptide comprising the amino acid sequence set forth as ILGV-LTSLV (SEQ ID NO: 2);

(b) a Neuropilin 1 (NRP1) polypeptide comprising the amino acid sequence set forth as GX₄LGMVSG (SEQ ID NO: 7), wherein X₄ is a leucine (L) or a methionine (M); and

(c) a Tumor Endothelial Marker 1 (TEM1) polypeptide comprising the amino acid sequence set forth as

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LLVPTCVFX₅V (SEQ ID NO: 9), wherein X₅ is a leucine (L) or a valine (V); and

contacting the cancer, with the activated CTLs or CTLs matured from the CTL precursors, wherein the cancer expresses DLK1, NRP1 and TEM1, thereby inhibiting the growth of the cancer.

9. The method of claim 8, wherein the cancer is a colorectal cancer.

10. The method of claim 8, wherein the plurality of polypeptides comprises:

(a) a Protein Delta Homolog 1 (DLK1) polypeptide comprising the amino acid sequence set forth as ILGV-LTSLV (SEQ ID NO: 2);

(b) a Neuropilin 1 (NRP1) polypeptide comprising the amino acid sequence set forth as GX₄LGMVSG (SEQ ID NO: 7), wherein X₄ is a methionine (M); and

(c) a Tumor Endothelial Marker 1 (TEM1) polypeptide comprising the amino acid sequence set forth as LLVPTCVFX₅V (SEQ ID NO: 9), wherein X₅ is a leucine (L).

11. The method of claim 8, wherein the cancer is lung cancer.

12. A method for eliciting an immune response to a tumor in a subject, comprising administering to a subject a therapeutically effective amount of a composition comprising a plurality of polypeptides, wherein each polypeptide in the plurality is at most twelve amino acids in length, wherein the plurality of polypeptides comprises:

(a) a Protein Delta Homolog 1 (DLK1) polypeptide comprising the amino acid sequence set forth as ILGV-LTSLV (SEQ ID NO: 2);

(b) a Neuropilin 1 (NRP1) polypeptide comprising the amino acid sequence set forth as GX₄LGMVSG (SEQ ID NO: 7), wherein X₄ is a leucine (L) or a methionine (M); and

(c) a Tumor Endothelial Marker 1 (TEM1) polypeptide comprising the amino acid sequence set forth as LLVPTCVFX₅V (SEQ ID NO: 9), wherein X₅ is a leucine (L) or a valine (V),

wherein the tumor expresses DLK1, NRP1 and TEM1 and wherein the tumor is a melanoma, thereby eliciting the immune response to the tumor.

13. The method of claim 12, wherein the melanoma is a superficial spreading melanoma, a nodular melanoma, an acral lentiginous melanoma, a lentigo maligna, a clear cell sarcoma, a mucosal melanoma or a uveal melanoma.

14. The method of claim 12, wherein the plurality of polypeptides comprises:

(a) a Protein Delta Homolog 1 (DLK1) polypeptide comprising the amino acid sequence set forth as ILGV-LTSLV (SEQ ID NO: 2);

(b) a Neuropilin 1 (NRP1) polypeptide comprising the amino acid sequence set forth as GX₄LGMVSG (SEQ ID NO: 7), wherein X₄ is a methionine (M); and

(c) a Tumor Endothelial Marker 1 (TEM1) polypeptide comprising the amino acid sequence set forth as LLVPTCVFX₅V (SEQ ID NO: 9), wherein X₅ is a leucine (L).

15. The method of claim 14, further comprising administering to the subject a therapeutically effective amount of dasatinib.

16. A method for inhibiting the growth of a cancer cell, the method comprising

culturing cytotoxic T lymphocytes (CTLs) or CTL precursor cells with a composition and an antigen presenting cell in vitro to produce activated CTLs or CTL matured from the CTL precursors that recognize tumor associ-

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ated stromal cell antigens, wherein the composition comprises a plurality of polypeptides, wherein each polypeptide in the plurality is at most twelve amino acids in length, wherein the plurality of polypeptides comprises:

- (a) a Protein Delta Homolog 1 (DLK1) polypeptide comprising the amino acid sequence set forth as ILGV-LTSLV (SEQ ID NO: 2);
 - (b) a Neuropilin 1 (NRP1) polypeptide comprising the amino acid sequence set forth as GX₄LGMVSG (SEQ ID NO: 7), wherein X₄ is a leucine (L) or a methionine (M); and
 - (c) a Tumor Endothelial Marker 1 (TEM1) polypeptide comprising the amino acid sequence set forth as LLVPTCVFX₅V (SEQ ID NO: 9), wherein X₅ is a leucine (L) or a valine (V); and
- contacting the cancer, with the activated CTLs or CTLs matured from the CTL precursors, thereby inhibiting the growth of the cancer, wherein the cancer expresses DLK1, NRP1 and TEM1 and is a melanoma.

17. The method of claim **16**, wherein the melanoma is a superficial spreading melanoma, a nodular melanoma, an acral lentiginous melanoma, a lentigo maligna, a clear cell sarcoma, a mucosal melanoma or a uveal melanoma.

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